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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 06:09:02 ; Search time 6028 Seconds
(without alignments)
10590.759 Million cell updates/sec

Title: US-10-089-364-3
Perfect score: 1350
Sequence: 1 atgtgtgcagtcctccgcctc.....ggggcgagtgatttgcctag 1350

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1347	99.8	1404	6 A19452	A19452 phytase cDN
2	1347	99.8	1404	6 I13430	I13430 Sequence 33
3	1347	99.8	1404	6 I33881	I33881 Sequence 19
4	1347	99.8	1404	6 AR195149	AR195149 Sequence
5	1347	99.8	2000	8 ANPHVAG	Z16414 Aspergillus
6	1347	99.8	2665	8 ANPHYTASE	M44550 Aspergillus
7	1347	99.8	6756	6 A19451	A19451 phytase gen
8	1347	99.8	6756	6 I13429	I13429 Sequence 31
9	1347	99.8	6756	6 AR195148	AR195148 Sequence
10	1275	94.4	2363	6 AR018076	AR018076 Sequence
11	1275	94.4	2363	6 AR051916	AR051916 Sequence
12	1275	94.4	2379	6 AR053934	AR053934 Sequence
13	1275	94.4	2379	8 ANPHYTAS	L0421 Aspergillus
14	1270.2	94.1	1525	8 A426977	A426977 Aspergill
15	1268.6	94.0	1528	8 AR218813	AR218813 Aspergill
16	1204.6	89.2	1506	8 AY513749	AY513749 Aspergill
17	1188.6	88.0	1347	8 AF537344	AF537344 Aspergill
18	1185.4	87.8	1590	8 AY013315	AY013315 Aspergill
19	1183.8	87.7	1347	8 AY603416	AY603416 Aspergill

20	1183.8	87.7	1347	8 AY615712	AY615712 Aspergill
21	1182.2	87.6	1515	6 AR116878	AR116878 Sequence
22	1182.2	87.6	1515	6 AR175871	AR175871 Sequence
23	1182.2	87.6	1515	6 AR306351	AR306351 Sequence
24	1182.2	87.6	1515	8 AB022700	AB022700 Aspergill
25	1182	87.6	1350	12 AF353576	AF353576 Synthetic
26	1167.2	86.5	1332	6 AR116877	AR116877 Sequence
27	1167.2	86.5	1332	6 AR175870	AR175870 Sequence
28	1167.2	86.5	1332	6 AR306350	AR306350 Sequence
29	1152.6	85.4	1335	6 AX960554	AX960554 Sequence
30	1119	82.9	1335	6 AX960552	AX960552 Sequence
31	1111	82.3	1335	6 AX960550	AX960550 Sequence
32	1104.2	81.8	1350	12 AR293525	AR293525 Synthetic
33	1075	79.6	1404	12 AX150806	AX150806 Synthetic
34	841	62.3	1347	12 AF542235	AF542235 Synthetic
35	810.4	60.0	1912	6 A46793	A46793 Sequence 11
36	810.4	60.0	1912	6 AR170094	AR170094 Sequence
37	810.4	60.0	1912	6 AR201125	AR201125 Sequence
38	810.4	60.0	1912	6 AR481763	AR481763 Sequence
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44	741.2	54.9	1434	12 AV182954	AV182954 Synthetic
45	659.8	48.9	1426	6 BD243286	BD243286 Improved

ALIGNMENTS

RESULT 1
A19452 LOCUS A19452 1404 bp RNA linear PAT 10-JUN-1994
DEFINITION Phytase cDNA fragment.
ACCESSION A19452
VERSION A19452.1 GI:583195
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Veenstra, A.E., Luiten, R.G.M. and Selten, G.C.M.
TITLE Cloning and expression of microbial phytase
JOURNAL Patent: EP 0420358-A 41 03-APR-1991;
GIST-BROCADES N.V.
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Location/Qualifiers
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KLSPCDLFDHEDWNYDLQSLKXYGHCAGNPLGTCQGVANGELARLTHSPVHD
DISSNHTLSSPATPLNSTLYADFSHDNGIISILFALGNGTKEPLSTTVENTTQT
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ORIGIN
Query Match 99.8%; Score 1347; DB 6; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2.9e-291;

Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCCCGCTCGAGAAATCAATCCAGTTCGGATACGGTGCATCAGGGGTATCAA 63
Db CTGGCAGTCCCCCGCTCGAGAAATCAATCCAGTTCGGATACGGTGCATCAGGGGTATCAA 117

QY 64 TGTCTTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 123
Db TGTCTTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 177

QY 124 GAATCGGTATCTCCCTGAGTGCCTCGCGGATGCAGAGTCACTTCGCTCAGTCTCTC 183
Db GAATCGGTATCTCCCTGAGTGCCTCGCGGATGCAGAGTCACTTCGCTCAGTCTCTC 237

QY 184 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 243
Db TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 297

QY 244 GAGGAGATCCAGCAACCGGACCGTTCGAGGAAATATGCTTCTCGAGGACATAC 303
Db GAGGAGATCCAGCAACCGGACCGTTCGAGGAAATATGCTTCTCGAGGACATAC 357

QY 304 AACTACAGTTCGGGTGCAGATGACCTGACTCCCTTCGAGAAACAGGAGTAGTCAACTCC 363
Db AACTACAGTTCGGGTGCAGATGACCTGACTCCCTTCGAGAAACAGGAGTAGTCAACTCC 417

QY 1024 TCGATGACACGGGATCATCTCCATCTCTTTTGTGTTAGTCTGTGACAGGCACTTAAG 1083
Db TCGATGACACGGGATCATCTCCATCTCTTTTGTGTTAGTCTGTGACAGGCACTTAAG 1137

QY 1084 CGCTATCTACCAACGACCGTTCGAGAAATATCAACCAAGATGAGATTCCTGCTCTGG 1143
Db CGCTATCTACCAACGACCGTTCGAGAAATATCAACCAAGATGAGATTCCTGCTCTGG 1197

QY 1144 ACGGTTCCGTTTGTCTCGGTTTGTACGTCGAGATGATGACAGTGTCCAGCGGAGCAGGAG 1203
Db ACGGTTCCGTTTGTCTCGGTTTGTACGTCGAGATGATGACAGTGTCCAGCGGAGCAGGAG 1257

QY 1204 CGCTCGTCCGTTGTCTTGTAAATGATCCGTTGTCGCCCTGCATGGGTTCCGGTTGAT 1263
Db CGCTCGTCCGTTGTCTTGTAAATGATCCGTTGTCGCCCTGCATGGGTTCCGGTTGAT 1317

QY 1264 GCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1323
Db GCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1377

QY 1324 GGTGATGGCGGAGTGTCTTTGCTTAG 1350
Db GGTGATGGCGGAGTGTCTTTGCTTAG 1404

RESULT 2
I13430
LOCUS
DEFINITION Sequence 33 from patent US 5436156.
ACCESSION I13430
VERSION I13430.1 GI:910771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.A.,
Veenstra,A.E., Luiten,R.G.M. and Selden,G.C.M.
TITLE Cloning and expression of phytase from *aspergillus*
JOURNAL Patent: US 5436156-A 33 25-JUL-1995;
FEATURES
Location/Qualifiers
source
1. .1404
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 99.8%; Score 1347; DB 6; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2.9e-251;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCCCGCTCGAGAAATCAATCCAGTTCGGATACGGTGCATCAGGGGTATCAA 63
Db CTGGCAGTCCCCCGCTCGAGAAATCAATCCAGTTCGGATACGGTGCATCAGGGGTATCAA 117

QY 64 TGTCTTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 123
Db TGTCTTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 177

QY 124 GAATCGGTATCTCCCTGAGTGCCTCGCGGATGCAGAGTCACTTCGCTCAGTCTCTC 183
Db GAATCGGTATCTCCCTGAGTGCCTCGCGGATGCAGAGTCACTTCGCTCAGTCTCTC 237

QY 184 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 243
Db TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 297

QY 244 GAGGAGATCCAGCAACCGGACCGTTCGAGGAAATATGCTTCTCGAGGACATAC 303
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QY 304 AACTACAGTTCGGGTGCAGATGACCTGACTCCCTTCGAGAAACAGGAGTAGTCAACTCC 363
Db AACTACAGTTCGGGTGCAGATGACCTGACTCCCTTCGAGAAACAGGAGTAGTCAACTCC 417

QY 364 GGCATCAAGTTCACCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATGCTTCTCGA 423
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418 GGCAATCAAGTTCTACGAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTTCATCCGA 477
424 TCCTCTGGCTCCAGCGCGGTGCTCGGCAAGAAATTCATCAGGGCTTCCAGAGC 483
478 TCCTCTGGCTCCAGCGCGGTGCTCGGCAAGAAATTCATCAGGGCTTCCAGAGC 537
484 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCAATTCGTCGCCCAAGATCGACGTGGTC 543
538 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCAATTCGTCGCCCAAGATCGACGTGGTC 597
544 ATTTCCAGGGCAGCTCATTCACACACACTCTCGACCCAGGACCTGCACTGCTTCGAA 603
598 ATTTCCAGGGCAGCTCATTCACACACACTCTCGACCCAGGACCTGCACTGCTTCGAA 657
604 GACAGCAATTTGGCCGATACCGTTCGAAGCAATTTACCGCCACGTTTCGTCCTCCATT 663
658 GACAGCAATTTGGCCGATACCGTTCGAAGCAATTTACCGCCACGTTTCGTCCTCCATT 717
664 CGTCAAGCTGAGAGACGACTGTCGGGTGTGACTCTACACACAGAAAGTGAAGTAC 723
718 CGTCAAGCTGAGAGACGACTGTCGGGTGTGACTCTACACACAGAAAGTGAAGTAC 777
724 CTGATGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTTCGACACCAAGCTGTCC 783
778 CTGATGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTTCGACACCAAGCTGTCC 837
784 CCCTTCTGTGACCTGTTTCAACCATGACGAATGAGATCAACTACGACTACCTCCAGTCTTG 843
838 CCCTTCTGTGACCTGTTTCAACCATGAGATGAGATCAACTACGACTACCTCCAGTCTTG 897
844 AAAAGTATTACGGCCATGTGAGGTAAACCGCTCGGCGCGACCCAGGGCGTGGCTAC 903
898 AAAAGTATTACGGCCATGTGAGGTAAACCGCTCGGCGCGACCCAGGGCGTGGCTAC 957
904 GCTAACAGGCTCATGCGCGCTGACCCACTCGGCTGTCCACGATGACACAGTTCACAC 963
958 GCTAACGAGCTCATGCGCGCTGACCCACTCGGCTGTCCACGATGACACAGTTCACAC 1017
964 CACATTTGAGCTCGAGCGGGTACCTTTCCGCTGAACTCTACTCTCTACGGCGACTTT 1023
1018 CACATTTGAGCTCGAGCGGGTACCTTTCCGCTGAACTCTACTCTCTACGGCGACTTT 1077
1024 TCAGATGACAAAGGATCATCTCCATTCTCTTTCTTTTGTGCTGTGTAACAGGCACTAAG 1083
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1138 CCGCTATCTACCAAGCGGTGAGAAATATCACACAGATGAGATCTCTGCTGTGG 1197
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1198 ACGGTTCCGTTTGTCTCGGTTTGTACGTGAGATGATGAGTGTACAGGCGGAGAGAG 1257
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1264 GCTTTGGGAGATGATCCGGGATGATTTGTTGAGGGGTTGAGCTTTGATGATCTGGG 1323
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1378 GGTGATTGGGCGGAGTGTGTTGCTTAG 1404

RESULT 3
LOCUS I33881 1404 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 19 from patent US 5593963.
ACCESSION I33881
VERSION I33881.1 GI:1824672

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Van Ooijen,A.J.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C.
and Verwoerd,T.C.
TITLE Expression of phytae in plants
JOURNAL Patent: US 5593963-A 19 14-JAN-1997;
FEATURES
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ORIGIN
Query Match 99.8%; Score 1347; DB 6; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2.9e-291;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTTCGGATACGGTTCGATCAGGGGTATCAA 63
DB 58 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTTCGGATACGGTTCGATCAGGGGTATCAA 117
QY 64 TCCTTCTCGAGACTTCGCATCTTTGGGTCAATACGACACCGTTCTTCTCTGCGCAAC 123
DB 118 TCCTTCTCGAGACTTCGCATCTTTGGGTCAATACGACACCGTTCTTCTCTGCGCAAC 177
QY 124 GAATCGGTATCTCCCTGAGGTGCCCGCGGATCGAGATCACTTTTCGTCAGTCTCTC 183
DB 178 GAATCGGTATCTCCCTGAGGTGCCCGCGGATCGAGATCACTTTTCGTCAGTCTCTC 237
QY 184 TCCGCTCATGAGCGGTATCCGACCGACTCCAGGGCAAGAAATATCTCCGCTCTCAT 243
DB 238 TCCGCTCATGAGCGGTATCCGACCGACTCCAGGGCAAGAAATATCTCCGCTCTCAT 297
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DB 298 GAGGAGATCCAGCAAGACCGCACCTTTTTCGCGAAATATGCTTCTCTGAGACATAC 357
QY 304 AACTCAGTTTGGGTGAGATGACCTGACTCCCTTCGGAGACAGAGGTAGTCACTCC 363
DB 358 AACTCAGTTTGGGTGAGATGACCTGACTCCCTTCGGAGACAGAGGTAGTCACTCC 417
QY 364 GCATCAAGTTCTTACAGCGGTACGAATCGCTCACAAGAAACATCGTTCCATTTCATCCGA 423
DB 418 GGCATCAAGTTCTTACAGCGGTACGAATCGCTCACAAGAAACATCGTTCCATTTCATCCGA 477
QY 424 TCCTTGGCTTCAGCGCGGTGATCGCTTCGGCAAGAAATTCATCGAGGCTTCAGAGC 483
DB 478 TCCTTGGCTTCAGCGCGGTGATCGCTTCGGCAAGAAATTCATCGAGGCTTCAGAGC 537
QY 484 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCAATTCGTCGCCCAAGATCGACGTGGTC 543
DB 538 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCAATTCGTCGCCCAAGATCGACGTGGTC 597
QY 544 ATTTCCAGGGCAGCTCATTCACACACACTCTCGACCCAGGACCTGCACTGCTTCGAA 603
DB 598 ATTTCCAGGGCAGCTCATTCACACACACTCTCGACCCAGGACCTGCACTGCTTCGAA 657
QY 604 GACAGCAATTTGGCCGATACCGTTCGAAGCAATTTACCGCCACGTTTCGTCCTCCATT 663
DB 658 GACAGCAATTTGGCCGATACCGTTCGAAGCAATTTACCGCCACGTTTCGTCCTCCATT 717
QY 664 CGTCAAGCTGAGAGACGACTGTCGGGTGTGACTCTCAGACACAGAAAGTGAAGTAC 723
DB 718 CGTCAAGCTGAGAGACGACTGTCGGGTGTGACTCTCAGACACAGAAAGTGAAGTAC 777
QY 724 CTGATGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTTCGACACCAAGCTGTCC 783
DB 778 CTGATGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTTCGACACCAAGCTGTCC 837
QY 784 CCCTTCTGTGACCTGTTTCAACCATGAGATCAACTACGACTACCTCCAGTCTCTG 843

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Db      898  AAAAAAGTATTACGGCCATGTTGTCAGGTAAACCGGTGCGCCCGACCCAGAGGCGTTCGGCTAC  957
Qy      904  GCTAACGAGCTCATCGCCCGCTGTGACCCACTCGCTGTCCACGATGACACCAAGTTCACAAC  963
Db      958  GCTAACGAGCTCATCGCCCGCTGTGACCCACTCGCTGTCCACGATGACACCAAGTTCACAAC  1017
Qy      964  CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT  1023
Db      1018  CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT  1077
Qy      1024  TCGCATGACAAACGGGCATCATCTCCATTCTCTTTTCTTTAGGTCTGTACAACGGCACTAAG  1083
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Qy      1144  ACGGTTCCGCTTTGCTTTCGCGTTTGTAGCTCGAGATGATGAGTGTACGGGGAGCAGGAG  1203
Db      1198  ACGGTTCCGCTTTGCTTTCGCGTTTGTAGCTCGAGATGATGAGTGTACGGGGAGCAGGAG  1257
Qy      1204  CCGCTGCTCCGCTGCTTTGTTAAATGATCGCGTTCGCTGCGGATGATGATGATGATGAT  1263
Db      1258  CCGCTGCTCCGCTGCTTTGTTAAATGATCGCGTTCGCTGCGGATGATGATGATGATGAT  1317
Qy      1264  GCTTTGGGGAGATGATACCCGGATGATGTTGTTGATGATGATGATGATGATGATGATGAT  1323
Db      1318  GCTTTGGGGAGATGATACCCGGATGATGTTGTTGATGATGATGATGATGATGATGATGAT  1377
Qy      1324  GGTGATGGGGGAGTGTGTTGCTTAG  1350
Db      1378  GGTGATGGGGGAGTGTGTTGCTTAG  1404

RESULT 4
LOCUS      AR195149                      1404 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 33 from patent US 6350602.
ACCESSION  AR195149
VERSION     AR195149.1  GI:20244586
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1404)
AUTHORS   Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.Andreas.,
          Veenstra,A.Eveline., Luiten,R.G.M. and Seiten,G.C.M.
TITLE     Cloning and expression of phytase from aspergillus
JOURNAL   Patent: US 6350602-A 33 26-FEB-2002;
FEATURES   Location/Qualifiers
            source          1..1404
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ORIGIN
Query Match          99.8%; Score 1347; DB 6; Length 1404;
Best Local Similarity 100.0%; Pred. No. 2,9e-291;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  CTGCAGTCCCGGCTCGAGAAATCAATCCAGTTCGATACGATCGATCAGGGGTATCAA  63
Db      58  CTGCAGTCCCGGCTCGAGAAATCAATCCAGTTCGATACGATCAGGGGTATCAA  117
Qy      64  TGTCTTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC  123
Db      118  TGTCTTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCCTCTCTCTGCGCAAC  177
Qy      124  GAATCGGTGATCTCCCTCGAGGTGCCCGCGGATGACAGTCACTTTCGCTCAGGTCCTC  183
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Db      238  TCCGTCATGAGCGCGGTATCCGACCGACTCAAAGGCAAGAAATATCTCGCTCTCAAT  297
Qy      244  GAGGAGATCCAGAGAACCGGACCACTTTGACGGAATATGCTTCTCTGAGGACATAC  303
Db      298  GAGGAGATCCAGAGAACCGGACCACTTTGACGGAATATGCTTCTCTGAGGACATAC  357
Qy      304  AACTACAGCTTGGGTGAGATGACCTGATCCCTTCGGAGAACAGAGTAGTCAACTCC  363
Db      358  AACTACAGCTTGGGTGAGATGACCTGATCCCTTCGGAGAACAGAGTAGTCAACTCC  417
Qy      364  GGCATCAAGTTTACACAGGGTACGAATCGCTCAAGGAACATGTTCCATTCGGA  423
Db      418  GGCATCAAGTTTACACAGGGTACGAATCGCTCAAGGAACATGTTCCATTCGGA  477
Qy      424  TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCAAGAAATTCATCGAGGGTTCAGAGC  483
Db      478  TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCAAGAAATTCATCGAGGGTTCAGAGC  537
Qy      484  ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCCAATCGTCCGCCAAGATCGAGTGT  543
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Qy      604  GACACGAAATTTGGCGGATACCGTCGAAGCCAAATTTACCGCCCAAGATCGTCCCT  663
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Db      718  CGTCAACGCTGGAGAACGACCTGTCGCGGTGTGACTCTCAGACACACAGAGTAGCT  777
Qy      724  CTCATGAGATGTGCTCTCTCGACACCATCTCCACGACACCGTTCGACACCAAGCT  783
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Qy      784  CCTTCTGTGACCTGTTCAACCGATGAGAAATGATGATGATGATGATGATGATGATG  843
Db      838  CCTTCTGTGACCTGTTCAACCGATGAGAAATGATGATGATGATGATGATGATGATG  897
Qy      844  AAAAAAGTATTACGGGCATGTTGTCAGGTAAACCGGTGCGCCCGACCCAGGGGCT  903
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Qy      904  GCTAACGAGCTCATCGCCCGCTGTGACCCACTCGCTGTCCACGATGACACCAAGT  963
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Qy      964  CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTCTACGCG  1023
Db      1018  CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTCTACGCG  1077
Qy      1024  TCGCATGACAAACGGGCATCATCTCCATTCTCTTTTCTTTAGGTCTGTACAACGG  1083
Db      1078  TCGCATGACAAACGGGCATCATCTCCATTCTCTTTTCTTTAGGTCTGTACAACGG  1137
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ORGANISM Aspergillus niger
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J.,
Suykerbuyk, M.E.G., Luitzen, R.G.M., Van Paridon, P.A., Sellen, G.C.M.,
Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.
Cloning, molecular characterization and overexpression of the
phytase gene (phyA) of Aspergillus niger
Gene (1992) In press
2 (bases 1 to 2000)
van Hartingsveldt, W.
Direct Submission
Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical
Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands
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 1 (bases 1 to 2665)
 Mullaney, E.J., Gibbs, D.M. and Ullah, A.H.
 Positive identification of a lambda gt11 clone containing a region of fungal phytase gene by immunoprobe and sequence verification
 Appl. Microbiol. Biotechnol. 35 (5), 611-614 (1991)
 JOURNAL 9200601
 MEDLINE 1369340
 PUBMED 1369340
 2 (bases 1 to 2665)
 Mullaney, E.J.
 Sequence of the Aspergillus niger (ficum) phytase gene
 JOURNAL Unpublished (1992)
 COMMENT Original source text: Aspergillus niger (library: EMBL 3; NRRL 3135) DNA.

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ACCESSION	AR195148		
VERSION	AR195148.1 GI:20244585		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	Van Gormom, R.F.M., Van Hartingsveldt, W., Van Paridon, P. Andreas., Veenstra, A. Eveline., Luiten, R.G.M. and Seiten, G.C.M.		
TITLE	Cloning and expression of phytase from aspergillus		
JOURNAL	Patent: US 6350602-A 31 26-FEB-2002;		
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DEFINITION	Sequence 7 from patent US 5780292.		
ACCESSION	AR018076		
VERSION	AR018076.1 GI:3973679		
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REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2363) Nevalainen, H. K. M., Paloheimo, M. T., Miettinen-Oinonen, A. S. K., Torkkeli, T. K., Cantrell, M., Piddington, C. S., Rambosek, J. A., Turunen, M. K. and Fagerstrom, R. B.		

TITLE Production of phytate degrading enzymes in trichoderma
JOURNAL Patent: US 5760292-A 7 14-JUL-1998;
FEATURES Location/Qualifiers

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RESULT 11

AR051916 2363 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 7 from patent US 5830733.
DEFINITION AR051916
ACCESSION AR051916
VERSION AR051916.1 GI:5975280
KEYWORDS SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2363)
Nevalainen,H.K.M., Paloheimo,M.T., Miettinen-Oinonen,A.S.K.,
Torckeli,T.K., Cantrell,M., Piddington,C.S., Rambosek,J.A.,
Turunen,M.K., Fagerstrom,R.B. and Houston,C.S.
TITLE Nucleic acid molecules encoding phytase and ph2.5 acid phosphatase
JOURNAL Patent: US 5830733-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
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ORIGIN

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RESULT 14
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DEFINITION Aspergillus niger strain N14* phytase (phyA) gene, complete cds.
ACCESSION AY426977
VERSION AY426977.1 GI:38018638
KEYWORDS Aspergillus niger
SOURCE Aspergillus niger
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 1525)
Peng,Y.Y., Zhou,Z.Y. and Ma,L.P.
Cloning and characterization of phytase gene of Aspergillus niger
N14*
Unpublished
2 (bases 1 to 1525)
Peng,Y.Y., Zhou,Z.Y. and Ma,L.P.
Direct Submission
Submitted (01-OCT-2003) College of Animal Science & Technology,
Southwest Agricultural University, Hiansheng, Beibei, Chongqing
400716, P.R. China
Location/Qualifiers
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ORIGIN

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precursor, gene, complete cds.
ACCESSION AF218813
VERSION AF218813.1 GI:6694940
KEYWORDS
SOURCE Aspergillus niger

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ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 1528)
AUTHORS Hongning, W., Qi, W. and Jing, X.
TITLE PCR, cloning and characterization of the phytase (phyA) gene of
Aspergillus niger (China Strain)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1528)
AUTHORS Hongning, W., Qi, W. and Jing, X.
TITLE Direct Submission
JOURNAL Submitted (24-DEC-1999) Aniaml Sci. & Tech. College, Sichuan
Agricultural University, Ya'an City, Sichuan Province 625014,
P.R.China
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Best Local Similarity 96.4%; Pred. No. 1.1e-273;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 06:11:07 ; Search time 728 Seconds
(without alignments)
9734.503 Million cell updates/sec

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Perfect score: 1350

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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseq1990s.*

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4: Geneseq2001as.*

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10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1347	99.8	1404	2 AAZ27421	Aaz27421 A. ficcum
5	1347	99.8	1506	6 ABN85588	Abn85588 Aspergill
6	1347	99.8	2665	12 ADL91241	Adl91241 Wild-type
7	1347	99.8	6756	2 AAQ11174	Aaql1174 Sequence,
8	1347	99.8	6756	2 AAT65137	Aat65137 Aspergill
9	1347	99.8	6756	8 ABX13436	Abx13436 Plasmids
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24	1343.8	99.5	2665	12 ADL91281	Adl91281 Mutant ph
25	1343.8	99.5	2665	12 ADL91255	Adl91255 Mutant ph
26	1343.8	99.5	2665	12 ADL91271	Adl91271 Mutant ph
27	1343.8	99.5	2665	12 ADL91279	Adl91279 Mutant ph
28	1343.8	99.5	2665	12 ADL91275	Adl91275 Mutant ph
29	1342.4	99.4	1344	6 ABN85591	Abn85591 Aspergill
30	1342.2	99.4	2665	12 ADL91277	Adl91277 Mutant ph
31	1342.2	99.4	2665	12 ADL91291	Adl91291 Mutant ph
32	1342.2	99.4	2665	12 ADL91283	Adl91283 Mutant ph
33	1342.2	99.4	2665	12 ADL91289	Adl91289 Mutant ph
34	1342.2	99.4	2665	12 ADL91285	Adl91285 Mutant ph
35	1340.6	99.3	2665	12 ADL91293	Adl91293 Mutant ph
36	1340.6	99.3	2665	12 ADL91287	Adl91287 Mutant ph
37	1337.4	99.1	2665	12 ADL91295	Adl91295 Mutant ph
38	1275	94.4	2363	2 AAQ58126	Aaqs58126 Phytase g
39	1275	94.4	2379	2 AAQ56944	Aaqs56944 A. niger
40	1185.4	87.8	1590	12 ADK90935	Adk90935 Aspergill
41	1182	87.6	1350	4 AAD03282	Aad03282 Aspergill
42	1182	87.6	1449	4 AAD03286	Aad03286 Carrot ex
43	1166.2	86.4	1515	2 AAT96709	Aat96709 Aspergill
44	1152.6	85.4	1335	12 ADF43256	Adf43256 Modified
45	1119	82.9	1335	12 ADF43254	Adf43254 Modified

ALIGNMENTS

RESULT 1
AAD03283
ID AAD03283 standard; DNA; 1350 BP.
XX
AC AAD03283;
XX
DT 13-JUN-2001 (first entry)
XX
DE Aspergillus niger phytase (Phy) A-1 gene.
XX
KW Phytase A; Phy; plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate; ds.
XX
OS Aspergillus niger.
XX
FH Key Location/Qualifiers
CDS
FT 1..1350
FT /*tag= a
FT /product= "Aspergillus niger phytase A-1 protein"
XX
PN WO200122806-A1.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-AU001183.
XX
PR 24-SEP-1999; 99AU-00003049.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUMO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX
Richardson AE, Hayes JE, Simpson RJ;
WPI: 2001-244964/25.
DR P-PSDB; AAY72974.
XX
PT New isolated nucleic acid encoding a mature phytase polypeptide for
enhancing the phosphorus nutrition of a plant, the growth of a plant on a
phosphorus source and the phosphorus content of a plant.
XX
PS Claim 7; Page 121-124; 144pp; English.
XX
CC The invention relates to a method of modifying plant productivity which

CC involves expressing phytase (Phy) A gene from *Aspergillus niger*, in a
CC plant cell. Phytase gene is capable of facilitating plants ability to
CC utilise soil phosphorus. It is used to enhance the phosphorus nutrition
CC of a plant or the growth of a plant on a phosphorus source comprising
CC phytate and/or increase the phosphorus content of a plant. This gene is
CC used to enhance the biomass produced by a plant and also to enhance the
CC rate of hypocotyl production or the rate of epicotyl production.
CC transgenic plant containing phytase gene has improved productivity than
CC its isogenic counterparts. The present sequence is *Aspergillus niger* Phy
CC A-1 gene. This gene is modified (Phy A-2 gene) in order to bring about
CC suitable expression in plant cells
XX
SQ Sequence 1350 BP; 288 A; 419 C; 332 G; 311 T; 0 U; 0 Other;

Query Match 100.0%; Score 1350; DB 4; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGCATCGGTGCGATCAGGGGTAT 60
DB 1 ATGCTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGCATCGGTGCGATCAGGGGTAT 60

QY 61 CAATGCTTCTCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCCTCTCTCGCA 120
DB 61 CAATGCTTCTCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCCTCTCTCGCA 120

QY 121 AACGAATCGGTTCATCTCCCTGAGTGCCTCCCGGATCGAGATCACTTTGCTCAGGTC 180
DB 121 AACGAATCGGTTCATCTCCCTGAGTGCCTCCCGGATCGAGATCACTTTGCTCAGGTC 180

QY 181 CTCTCCCTCATGAGCGCGTATCCGACCGACTCCAGGCAAGAAATCTCCGCTCTC 240
DB 181 CTCTCCCTCATGAGCGCGTATCCGACCGACTCCAGGCAAGAAATCTCCGCTCTC 240

QY 241 ATTGAGGAGTCCAGCAACGCGACCACTTTGAGGAAATATGCTTCTCGAAGACA 300
DB 241 ATTGAGGAGTCCAGCAACGCGACCACTTTGAGGAAATATGCTTCTCGAAGACA 300

QY 301 TACAACTACAGTTGGGTGCGAGATGACCTGCTCCCTCCGCAAGAAATTCATCGAGGGTTC 480
DB 301 TACAACTACAGTTGGGTGCGAGATGACCTGCTCCCTCCGCAAGAAATTCATCGAGGGTTC 480

QY 361 TCCGCGATCAAGTTCTACAGGGTACGAATCGTTCACAGGACATCGTTCATTCATC 420
DB 361 TCCGCGATCAAGTTCTACAGGGTACGAATCGTTCACAGGACATCGTTCATTCATC 420

QY 421 CGATCTCTGGCTCCAGCGCGGTGATCGCTCCGCAAGAAATTCATCGAGGGTTC 480
DB 421 CGATCTCTGGCTCCAGCGCGGTGATCGCTCCGCAAGAAATTCATCGAGGGTTC 480

QY 481 AGCACAAGCTGAAGATCTCTGTCGCGAGCGCGCCGATCGTCCGCAAGATCGAGTG 540
DB 481 AGCACAAGCTGAAGATCTCTGTCGCGAGCGCGCCGATCGTCCGCAAGATCGAGTG 540

QY 541 GTCAATTCGAGGCGAGTTCATCAACAACTCTCGACCCAGGACCTGCACTGTCTTC 600
DB 541 GTCAATTCGAGGCGAGTTCATCAACAACTCTCGACCCAGGACCTGCACTGTCTTC 600

QY 601 GAAGACAGCAATTTGGCCGATACCGTTCGAAGCAATTTCAACCGCAAGTTCGTCCTCC 660
DB 601 GAAGACAGCAATTTGGCCGATACCGTTCGAAGCAATTTCAACCGCAAGTTCGTCCTCC 660

QY 661 ATTCTGTCAGCTCTGGAGACGACTGTCGCTGCTGCTCTCAGACACAGAGTAC 720
DB 661 ATTCTGTCAGCTCTGGAGACGACTGTCGCTGCTGCTCTCAGACACAGAGTAC 720

QY 721 TACCTCATGGACATGTCTCTCGACACCACTCTCCACGACCGTCGACCAAGAGTG 780
DB 721 TACCTCATGGACATGTCTCTCGACACCACTCTCCACGACCGTCGACCAAGAGTG 780

QY 781 TCCCTCTCTGACCTGTTCCCTCATGACGATGATCACTACGACTACCTCAGTCC 840
DB 781 TCCCTCTCTGACCTGTTCCCTCATGACGATGATCACTACGACTACCTCAGTCC 840

QY 841 TTGAAGAATATTACGGCCATCGTTCAGTAAACCGCTCGGCCGACCCAGGGCGTCCGC 900
DB 841 TTGAAGAATATTACGGCCATCGTTCAGTAAACCGCTCGGCCGACCCAGGGCGTCCGC 900

QY 901 TAGCGTTAACAGACTCATCGCCGCTCTGACCCACTCGCTGTCCAGATGACACAGTTCC 960
DB 901 TAGCGTTAACAGACTCATCGCCGCTCTGACCCACTCGCTGTCCAGATGACACAGTTCC 960

QY 961 AACCACTTTGGATTCGAGCCGCTACCTTTCCGCTCAACTCTCTACGCGGAC 1020
DB 961 AACCACTTTGGATTCGAGCCGCTACCTTTCCGCTCAACTCTCTACGCGGAC 1020

QY 1021 TTTTCGCGATGACAACGGCATCATCTCCATTTCTTTTGTGTTTAGTCTCTCAACGGCACT 1080
DB 1021 TTTTCGCGATGACAACGGCATCATCTCCATTTCTTTTGTGTTTAGTCTCTCAACGGCACT 1080

QY 1081 AAGCGCTATCTACCAACGCGTGGAGATATCACCCAGACAGATGAGTTCTCTGCT 1140
DB 1081 AAGCGCTATCTACCAACGCGTGGAGATATCACCCAGACAGATGAGTTCTCTGCT 1140

QY 1141 TGGACGGTTCCGTTTGTGCTTTCGCGTTGTACGTGAGATGATGCACTGTCAGGCGAGCAG 1200
DB 1141 TGGACGGTTCCGTTTGTGCTTTCGCGTTGTACGTGAGATGATGCACTGTCAGGCGAGCAG 1200

QY 1201 GAGCGCTGGTCCGTTGCTTGTGTTAATGATCGCGTTGTCCGCTGCATGGGTGTCGGT 1260
DB 1201 GAGCGCTGGTCCGTTGCTTGTGTTAATGATCGCGTTGTCCGCTGCATGGGTGTCGGT 1260

QY 1261 GATGCTTTGGGAGATGATACCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCT 1320
DB 1261 GATGCTTTGGGAGATGATACCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCT 1320

QY 1321 GGGGGTGTATGGCGGAGTGTTCCTTAG 1350
DB 1321 GGGGGTGTATGGCGGAGTGTTCCTTAG 1350

RESULT 2
AAD03287
ID AAD03287 standard; DNA; 1449 BP.
XX
AC AAD03287;
XX
DT 11-SEP-2003 (revised)
DT 13-JUN-2001 (first entry)
XX
Carrot extensin leader peptide-A. niger phytase A-1 chimeric gene.
XX
Phytase A; Phy; plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate; carrot; extensin; ds.
XX
Daucus carota.
OS *Aspergillus niger*.
OS Chimeric.
XX
Key Location/Qualifiers
CDS 1..1449
FT /tag= a
FT /product= "Carrot extensin leader peptide-A. niger
FT phytase A-1 chimeric protein"
FT sig_peptide 1..100
FT /tag= b
FT /note= "Carrot extensin leader peptide"
FT mat_peptide 101..1446
FT /tag= c
FT /product= "Mature carrot extensin leader peptide- A.
FT niger phytase A-1 chimeric protein"
XX
WO200122806-A1.
XX
05-APR-2001.
PD

XX PF 22-SEP-2000; 2000WO-AU001183.
XX PR 24-SEP-1999; 99AU-00003049.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX Richardson AE, Hayes JE, Simpson RJ;
XX WPI; 2001-244964/25.
DR P-PSDB; AAY72978.
XX
PT New isolated nucleic acid encoding a mature phytase polypeptide for
PT enhancing the phosphorus nutrition of a plant, the growth of a plant on a
PT phosphorus source and the phosphorus content of a plant.
XX
PS Claim 9; Fig 1; 144pp; English.
XX
CC The invention relates to a method of modifying plant productivity which
CC involves expressing phytase (Phy) A gene from *Aspergillus niger*, in a
CC plant cell. Phytase gene is capable of facilitating plants ability to
CC utilise soil phosphorus. It is used to enhance the phosphorus nutrition
CC of a plant or the growth of a plant on a phosphorus source comprising
CC phytase and/or increase the phosphorus content of a plant. This gene is
CC used to enhance the biomass produced by a plant and also to enhance the
CC rate of hypocotyl production or the rate of epicotyl production.
CC Transgenic plant containing phytase gene has improved productivity than
CC its isogenic counterparts. The present sequence is carrot extensin leader
CC peptide-A. *niger* phytase A-1 chimeric gene. This chimeric gene is used to
CC enhance phosphorus nutrition in plants. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 1449 BP; 312 A; 439 C; 355 G; 343 T; 0 U; 0 Other;
Query Match 100.0%; Score 1350; DB 4; Length 1449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTAT 60
DB 100 ATGTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTAT 159
QY 61 CAATGCTTCTCGAGACTTCCATCTTTGGGGTCAATACGACCGCTTCTCTCTCTGCA 120
DB 160 CAATGCTTCTCGAGACTTCCATCTTTGGGGTCAATACGACCGCTTCTCTCTCTGCA 219
QY 121 AACGAATCGGTCACTCTCCCTGAGGTGCCCGCGGATGCGAGTCACTTTGCTCAGGTC 180
DB 220 AACGAATCGGTCACTCTCCCTGAGGTGCCCGCGGATGCGAGTCACTTTGCTCAGGTC 279
QY 181 CTCTCCCGTATGAGCGCGGTATCCGACCGACTCCAGGCGCAGAAATCTCCGCTCTC 240
DB 280 CTCTCCCGTATGAGCGCGGTATCCGACCGACTCCAGGCGCAGAAATCTCCGCTCTC 339
QY 241 ATTGAGGAGATCCAGCAGAACCGACCACTTTTGACCGGAAATATGCTTCTTCTGAAACA 300
DB 340 ATTGAGGAGATCCAGCAGAACCGACCACTTTTGACCGGAAATATGCTTCTTCTGAAACA 399
QY 301 TACAATCAAGTTGGTGGTGCATGACCTGCTCCCTTCGAGAACAGGAGCTAGTCAAC 360
DB 400 TACAATCAAGTTGGTGGTGCATGACCTGCTCCCTTCGAGAACAGGAGCTAGTCAAC 459
QY 361 TCGGCACTCAAGTTCTACCGCGGTACGAATCGCTCAAGGAACATCGTTCCATTTCATC 420
DB 460 TCGGCACTCAAGTTCTACCGCGGTACGAATCGCTCAAGGAACATCGTTCCATTTCATC 519
QY 421 CGATCTCTGCTCCAGCGCGGTGATCGCTCCCGCAAGAAATTCATCGAGGGTCCAG 480
DB 520 CGATCTCTGCTCCAGCGCGGTGATCGCTCCCGCAAGAAATTCATCGAGGGTCCAG 579
QY 481 AGCACCAGCTGAGGATCTCTGCTCCAGCGCGGCAATCGTCCGCCAGATCGAGTG 540

DB 580 AGCACCAAGCTGAAGGATCCTCGTCCCAAGCCCGCCAAATCGTCCGCCAAGATCGACGTC 639
QY 541 GTCAATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCACTGCTTTC 600
DB 640 GTCAATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCACTGCTTTC 699
QY 601 GAAGACAGCGAAATTTGGCCGATACCGTCGAAAGCAATTTTCCACGCCACGTTGCTCCCTCC 660
DB 700 GAAGACAGCGAAATTTGGCCGATACCGTCGAAAGCAATTTTCCACGCCACGTTGCTCCCTCC 759
QY 661 ATTCTGTCACGCTGAGAACGACCTGTCGGGTGTGACTCTCACAGACACAGAGTGACC 720
DB 760 ATTCTGTCACGCTGAGAACGACCTGTCGGGTGTGACTCTCACAGACACAGAGTGACC 819
QY 721 TACCTCATGAGACATGTCCTTCCGACACCATCTCCACGACGACCGTCGACACCAAGCTG 780
DB 820 TACCTCATGAGACATGTCCTTCCGACACCATCTCCACGACGACCGTCGACACCAAGCTG 879
QY 781 TCCCTCTCTGACCTGTTTACCCATGAGCAATGATCACTACGACTACCTCCAGTCC 840
DB 880 TCCCTCTCTGACCTGTTTACCCATGAGCAATGATCACTACGACTACCTCCAGTCC 939
QY 841 TTGAAAAGATTATTCGCGCCATGTCGAGTAACCCGCTCGGCCGACCCAGGCGCTCGGC 900
DB 940 TTGAAAAGATTATTCGCGCCATGTCGAGTAACCCGCTCGGCCGACCCAGGCGCTCGGC 999
QY 901 TAGCTTAAAGAGCTATACGCCCTGTCACCCACTCGCTGTCCAGATGACACCAAGTTC 960
DB 1000 TAGCTTAAAGAGCTATACGCCCTGTCGACCCACTCGCTGTCCAGATGACACCAAGTTC 1059
QY 961 AACCAACATTTGAGACTCGAGCGCGGTACTTTCGCTCAACTCTCTCTCTACCGGAC 1020
DB 1060 AACCAACATTTGAGACTCGAGCGCGGTACTTTCGCTCAACTCTCTCTCTACCGGAC 1119
QY 1021 TTTTCGATGACAAACGCGCATCATCTCCATTCCTTTTGGTCTGTGTACACGCGCACT 1080
DB 1120 TTTTCGATGACAAACGCGCATCATCTCCATTCCTTTTGGTCTGTGTACACGCGCACT 1179
QY 1081 AAGCCGCTATCTACACGACCGTGGAGAAATATCACCCAGACAGATGGATTCGCTCTGCT 1140
DB 1180 AAGCCGCTATCTACACGACCGTGGAGAAATATCACCCAGACAGATGGATTCGCTCTGCT 1239
QY 1141 TGACCGGTTCCGCTTTCGCTTTCGCTTTCGCTGAGATGATGACGTCAGGCGGAGCAG 1200
DB 1240 TGACCGGTTCCGCTTTCGCTTTCGCTTTCGCTGAGATGATGACGTCAGGCGGAGCAG 1299
QY 1201 GAGCCGCTGCTGCTGCTTTCGCTTTCGCTTTCGCTGAGATGATGACGTCAGGCGGTT 1260
DB 1300 GAGCCGCTGCTGCTGCTTTCGCTTTCGCTTTCGCTGAGATGATGACGTCAGGCGGTT 1359
QY 1261 GATGCTTTGGGAGATGATACCGGGATAGCTTTGTGAGGGGGTTGAGCTTTCTAGATCT 1320
DB 1360 GATGCTTTGGGAGATGATACCGGGATAGCTTTGTGAGGGGGTTGAGCTTTCTAGATCT 1419
QY 1321 GGGGGTGTATTGGCGGAGTGTTCCTTAG 1350
DB 1420 GGGGGTGTATTGGCGGAGTGTTCCTTAG 1449
RESULT 3
AAQ11175
ID AAQ11175 standard; cDNA; 1404 BP.
XX
AC AAQ11175;
XX
XX 25-MAR-2003 (revised)
DT 30-MAR-2000 (revised)
DT 31-MAY-1991 (first entry)
XX
DE Chromosomal phytase encoding sequence.
XX
KW Microbial phytase; animal feed; inositol; inorganic phosphate; ss.
XX

OS Synthetic.
 XX Key Location/Qualifiers
 FH 1..1404
 FT /tag= a
 FT /product= "chromosomal phytase"
 FT 1..69
 FT sig_peptide /tag= b
 XX
 PN EP420358-A.
 XX
 PD 03-APR-1991.
 XX
 PF 27-SEP-1990; 90EP-00202565.
 XX
 PR 27-SEP-1989; 89EP-00202436.
 PR 17-AUG-1990; 90EP-00202231.
 XX
 XX (KONN) GIST-BROCADES NV.
 PA (STAM) DSM NV.
 XX
 PI Van Gorcom RP, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;
 PI Luiten RG, Seiten GCM;
 XX
 DR WPI; 1991-095799/14.
 DR P-PSDB; AAR11333.
 XX
 PT DNA encoding phytase - used for recombinant expression for prodn. of
 PT phytase for conversion of phytate to inositol and inorganic phosphate
 PT esp. in animal feed.
 XX
 PS Disclosure; Fig 8; 61pp; English.
 XX
 CC This sequence is the translation region deduced from comparisons of
 CC respective sequences of clones identified using oligonucleotide probes.
 CC The use of recombinant DNA methods for the the enzyme prodn. allows the
 CC large scale prodn. of proteins and peptides having phytase activity.
 CC These are used for the conversion of phytate to inositol and inorganic
 CC phosphate and can be used in industrial processes. The phosphate content
 CC of manure thus can be decreased. See also AAQ1157-74. (Revised record
 CC issued to correct errors present in the sequence portion of the original
 CC GENESQ entry.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 1404 BP; 293 A; 436 C; 344 G; 331 T; 0 U; 0 Other;
 Query Match 99.8%; Score 1347; DB 2; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4 CTGGCAGTCCCGCTCAGAGAAATCAATCCAGTTCGATCGATCGATCAGGGGTATCAA 63
 58 CTGGCAGTCCCGCTCAGAGAAATCAATCCAGTTCGATCGATCGATCAGGGGTATCAA 117
 64 TCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCCTCTCTCTCGCAAC 123
 118 TGTCTCTCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCCTCTCTCGCAAC 177
 124 GAATCGGTCACTCCCTGAGGTGCCCCCGGATGAGAGTCACTTTCGCTCAGGTCTTC 183
 178 GAATCGGTCACTCCCTGAGGTGCCCCCGGATGAGAGTCACTTTCGCTCAGGTCTTC 237
 184 TCCCGTCAATGAGCGGTATCCGACCGACTCCAGGCAAGAAATCTCCGCTCTCAT 243
 238 TCCCGTCAATGAGCGGTATCCGACCGACTCCAGGCAAGAAATCTCCGCTCTCAT 297
 244 GAGGAGATCCAGCAGACCGACCACTTTTCAGGAAATATGCTTCTTGAAGACATAC 303
 298 GAGGAGATCCAGCAGACCGACCACTTTTCAGGAAATATGCTTCTTGAAGACATAC 357
 304 AACTACAGTTGGGTGAGATGACCTGACTCCCTCCGAGAACAGGAGCTAGTCACTCC 363
 358 AACTACAGTTGGGTGAGATGACCTGACTCCCTCCGAGAACAGGAGCTAGTCACTCC 417

QY 364 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTTCATCCGA 423
 DB 418 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTTCATCCGA 477
 QY 424 TCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGTTCAGAGC 483
 DB 478 TCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGTTCAGAGC 537
 QY 484 ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTCCCAAGATCGAGTGTTC 543
 DB 538 ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTCCCAAGATCGAGTGTTC 597
 QY 544 ATTTCGAGGCCAGCTCATCCAAACAACTCTCGACCCAGGCACTGCACTGTCTTCGAA 603
 DB 598 ATTTCGAGGCCAGCTCATCCAAACAACTCTCGACCCAGGCACTGCACTGTCTTCGAA 657
 QY 604 GACAGCAATTGGCGGATACCGTCCGAAGCAATTTTCACCGCCACGTTTGGTCCCTTCATT 663
 DB 658 GACAGCAATTGGCGGATACCGTCCGAAGCAATTTTCACCGCCACGTTTGGTCCCTTCATT 717
 QY 664 CGTCAACGCTCTGAGAAACGACCTGTCGGTGTGACTCTCACAGACACAGAAAGTGCCTAC 723
 DB 718 CGTCAACGCTCTGAGAAACGACCTGTCGGTGTGACTCTCACAGACACAGAAAGTGCCTAC 777
 QY 724 CTCATGACATGTCTCTTCGACACCAATCTCCACAGACCGTTCGACACCAAGTGTTC 783
 DB 778 CTCATGACATGTCTCTTCGACACCAATCTCCACAGACCGTTCGACACCAAGTGTTC 837
 QY 784 CCTCTGTGACCTGTTCACCCATGACGAATGATCAACTAGACTACTCTCCAGTCCCTTG 843
 DB 838 CCTCTGTGACCTGTTCACCCATGACGAATGATCAACTAGACTACTCTCCAGTCCCTTG 897
 QY 844 AAAAGTATTACGGCATGTGTCAGGTAAACCGCTCGGCCGACCCAGGGGGTTCGGTAC 903
 DB 898 AAAAGTATTACGGCATGTGTCAGGTAAACCGCTCGGCCGACCCAGGGGGTTCGGTAC 957
 QY 904 GCTAACGACTATGCGCGGTGTGACCCACTGCGCTGTCCAGTACAGACAGTTCCTCAAC 963
 DB 958 GCTAACGACTATGCGCGGTGTGACCCACTGCGCTGTCCAGTACAGACAGTTCCTCAAC 1017
 QY 964 CACACTTTGGAATCGAGCCCGGTACTCTTTCGGCTCAACTCTACTCTCTACGGGACTTT 1023
 DB 1018 CACACTTTGGAATCGAGCCCGGTACTCTTTCGGCTCAACTCTACTCTCTACGGGACTTT 1077
 QY 1024 TGCATGACAAAGCATATCTCCATCTCTTTGCTTTAGTCTGTGTACACGGGACTTAAG 1083
 DB 1078 TGCATGACAAAGCATATCTCTCCATCTCTTTGCTTTAGTCTGTGTACACGGGACTTAAG 1137
 QY 1084 CCGCTATCTACCAAGCATGTCGAGAAATATCACCCAGACAGATGGATTTCTCGTCTCTGG 1143
 DB 1138 CCGCTATCTACCAAGCATGTCGAGAAATATCACCCAGACAGATGGATTTCTCGTCTCTGG 1197
 QY 1144 ACGGTTCCGTTTTCGTTGCGTTTACGTCGAGATGATGAGTGTGAGCGGAGAGAGAG 1203
 DB 1198 ACGGTTCCGTTTTCGTTGCGTTTACGTCGAGATGATGAGTGTGAGCGGAGAGAGAG 1257
 QY 1204 CCGCTGTCGCTGTCTTGGTTAATGATCGCTGTCCGCTCATGGGTGTCCGTTTGTAT 1263
 DB 1258 CCGCTGTCGCTGTCTTGGTTAATGATCGCTGTCCGCTCATGGGTGTCCGTTTGTAT 1317
 QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTTGTAGGGGGTTGAGTTTCTAGATCTCGG 1323
 DB 1318 GCTTTGGGAGATGTACCCGGGATAGCTTTTGTAGGGGGTTGAGTTTCTAGATCTCGG 1377
 QY 1324 GGTGATGGCGGAGTGTTCCTTAG 1350
 DB 1378 GGTGATGGCGGAGTGTTCCTTAG 1404

RESULT 4
 AA227421
 ID AA227421 standard; cDNA; 1404 BP.

XX AC AA227421;
 XX DT 27-AUG-2003 (revised)
 XX DT 07-DEC-1999 (first entry)
 XX DE A. ficum phytase coding sequence.
 XX KW Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 XX KW phytate level reduction; animal manure; food preparation; soy processing;
 XX KW inositol manufacture; ss.
 XX OS Aspergillus ficum.
 XX PN WO9949022-A1.
 XX PD 30-SEP-1999.
 XX PP 22-MAR-1999; 99WO-DK000153.
 XX PR 23-MAR-1998; 98DK-00000407.
 XX PR 19-JUN-1998; 98DK-00000806.
 XX PR 18-SEP-1998; 98DK-00001176.
 XX PR 22-JAN-1999; 99DK-00000091.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A;
 XX DR WPI; 1999-580444/49.
 XX DR P-PSDB; AAY39904.
 XX PT New variant phytase enzymes, used for liberating phosphorus from a
 XX PT phytase substrate, for reducing phytate levels in animal manure and in
 XX PT feed and food preparations.
 XX PS Disclosure; Fig 11; 141pp; English.
 XX CC This sequence encodes the Aspergillus ficum phytase sequence. The
 XX CC invention relates to variant phytase enzymes with specific amino acid
 XX CC substitutions for improved properties. The phytase variants can be used
 XX CC for liberating phosphorus from a phytase substrate. They can be used for
 XX CC reducing phytate levels in animal manure. They can be used in feed or
 XX CC food preparations. The phytase DNA can also be used to produce transgenic
 XX CC plants which can be used in feeds or foods. The phytase variants can also
 XX CC be used in soy processing and in the manufacture of inositol or
 XX CC derivatives. The phytase variants can have altered activities such as pH
 XX CC stability, temperature stability, pH profile, temperature profile,
 XX CC specific activity (in particular in relation to pH and temperature),
 XX CC substrate specificity, substrate cleavage pattern, substrate binding,
 XX CC position specificity, the velocity and level of release of phosphate from
 XX CC corn, reaction rate, phytase degradation rate and end level of released
 XX CC phosphate reached. (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 1404 BP; 293 A; 436 C; 344 G; 331 T; 0 U; 0 Other;
 Query Match 99.8%; Score 1347; DB 2; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CTGGAGTCCCGGCTCGAGAAATCAATCCAGTTGGATACGGTCGATCAGGGGTATCAA 63
 DB 58 CTGGAGTCCCGGCTCGAGAAATCAATCCAGTTGGATACGGTCGATCAGGGGTATCAA 117
 QY 64 TGCTTCTCCGAGACTTCGCACTTTGGGGTCAATACCGACCGTTCTTCTCTGGCAAC 123
 DB 118 TGCTTCTCCGAGACTTCGCACTTTGGGGTCAATACCGACCGTTCTTCTCTGGCAAC 177
 QY 124 GAATCGGTCACTCCCTCGAGGTGCCCGCGGATGACAGTCACTTTTCGTTCAGGTCTC 183
 DB 178 GAATCGGTCACTCCCTCGAGGTGCCCGCGGATGACAGTCACTTTTCGTTCAGGTCTC 237
 QY 184 TCCGTCATGAGCGCGGTATCCGACCGATCCCAAGGGCAAGAAATACTCCGTCCTCAT 243

DB 238 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCAT 297
 QY 244 GAGGAGATCCAGCAAGACGCGACCACTTTGACGGAAATATGCCTTCTCTGAGACATAC 303
 DB 298 GAGGAGATCCAGCAAGACGCGACCACTTTGACGGAAATATGCCTTCTCTGAGACATAC 357
 QY 304 AACTCAGCTTGGGTGTCAGATGACCTGATCCCTTCGGAGAACAGGAGTACTCACTCC 363
 DB 358 AACTCAGCTTGGGTGTCAGATGACCTGATCCCTTCGGAGAACAGGAGTACTCACTCC 417
 QY 364 GGCATCAAGTTCTACGAGCGGTACCAATCGTCAAGAGAACATGTTCCATTCATCCGA 423
 DB 418 GGCATCAAGTTCTACGAGCGGTACCAATCGTCAAGAGAACATGTTCCATTCATCCGA 477
 QY 424 TCCTCTGGCTCCAGCGCGGTGATCCGCTCCGGCAAGAAATTCATCAGAGGGCTTCAGAGC 483
 DB 478 TCCTCTGGCTCCAGCGCGGTGATCCGCTCCGGCAAGAAATTCATCAGAGGGCTTCAGAGC 537
 QY 484 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGGCCAATCGTGCGCCCAAGATCGAGTGGTC 543
 DB 538 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGGCCAATCGTGCGCCCAAGATCGAGTGGTC 597
 QY 544 ATTTCGAGGCGAGCTCACTCCAAACAACACTCTCGACCCAGGCACTGCACTCTCTTCGA 603
 DB 598 ATTTCGAGGCGAGCTCACTCCAAACAACACTCTCGACCCAGGCACTGCACTCTCTTCGA 657
 QY 604 GACAGGAATTCGCCGATACCGTTCGAAGCCAAATTTCAACGCCACCGTTCTGTCCTCCATT 663
 DB 658 GACAGGAATTCGCCGATACCGTTCGAAGCCAAATTTCAACGCCACCGTTCTGTCCTCCATT 717
 QY 664 CGTCAACGTCGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAGTAGTACCTAC 723
 DB 718 CGTCAACGTCGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAGTAGTACCTAC 777
 QY 724 CTCATGGACATGCTGCTTCGACACCATCTCCACAGCACCGTCCGACACCAAGGTGCC 783
 DB 778 CTCATGGACATGCTGCTTCGACACCATCTCCACAGCACCGTCCGACACCAAGGTGCC 837
 QY 784 CCCTTCTGTGACTGTTTACCCATGAGAAATGATGATCACTAGACTACTCTCAGTCTCTG 843
 DB 838 CCCTTCTGTGACTGTTTACCCATGAGAAATGATGATCACTAGACTACTCTCAGTCTCTG 897
 QY 844 AAAAAATATTACGGCCATGTCAGGTAAACCGCTCGCGCCAGCCAGCGGCTCGGCTAC 903
 DB 898 AAAAAATATTACGGCCATGTCAGGTAAACCGCTCGCGCCAGCCAGCGGCTCGGCTAC 957
 QY 904 GCTAACGAGCTCATCCCGCTGTGACCCACTCGCTGTCCAGATGACACCAAGTTCCAAAC 963
 DB 958 GCTAACGAGCTCATCCCGCTGTGACCCACTCGCTGTCCAGATGACACCAAGTTCCAAAC 1017
 QY 964 CACATTTGGACTCGAGCCCGGCTACCTTCGGCTCAACTCTACTCTCTACGCGACTTT 1023
 DB 1018 CACATTTGGACTCGAGCCCGGCTACCTTCGGCTCAACTCTACTCTCTACGCGACTTT 1077
 QY 1024 TCGCATGACACCGGATCATCTCCATTCTCTTTGGTTTAGGTCTGTACAAACGGCACTAAG 1083
 DB 1078 TCGCATGACACCGGATCATCTCCATTCTCTTTGGTTTAGGTCTGTACAAACGGCACTAAG 1137
 QY 1084 CGCTATCTACACACCGTGGAGAAATATCAACCCAGACAGATGATTTCTGCTCTCTTTGG 1143
 DB 1138 CGCTATCTACACACCGTGGAGAAATATCAACCCAGACAGATGATTTCTGCTCTCTTTGG 1197
 QY 1144 ACGGTTCCGTTTGGCTTTCGCTTGTACGTTCAGATGATGTCAGTGTCCAGCGGAGCAGAG 1203
 DB 1198 ACGGTTCCGTTTGGCTTTCGCTTGTACGTTCAGATGATGTCAGTGTCCAGCGGAGCAGAG 1257
 QY 1204 CGCTGGTCCGCTGTCTTGGTTAATGATCGGTGTGTCGCTGTGATGGGTGTCGCTTGTAT 1263
 DB 1258 CGCTGGTCCGCTGTCTTGGTTAATGATCGGTGTGTCGCTGTGATGGGTGTCGCTTGTAT 1317
 QY 1264 GCTTTGGGAGATGATACCCGGATAGCTTTGTGAGCGGGTTGAGCTTTGCTAGATCTGGG 1323

Db 1318 GCTTTGGGAGATGATACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 1377
QY 1324 GGTGATTGGGGAGTGTGTTTGTCTTAG 1350
Db 1378 GGTGATTGGGGAGTGTGTTTGTCTTAG 1404

RESULT 5
ABN8588
ID ABN8588 standard; DNA; 1506 BP.
XX
AC ABN8588;
XX
DT 17-SEP-2002 (first entry)
XX
DE Aspergillus niger phyA related polynucleotide 2.
XX
KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.
XX
OS Aspergillus niger.
XX
FH Key Location/Qualifiers
FT CDS 1..1506
FT /product= "phyA related protein"
FT /tag= a
FT exon 1..44
FT /tag= b
FT /number= 1
FT intron 45..146
FT /tag= c
FT /number= 1
FT exon 147..1506
FT /tag= d
FT /number= 2
XX
XX CN1333363-A.
XX
XX 30-JAN-2002.
XX
XX 12-JUL-2000; 2000CN-00117245.
XX
XX 12-JUL-2000; 2000CN-00117245.
XX
XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
XX
XX Chen Z, Yang L, Fang L;
XX
XX WPI; 2002-305615/35.
XX
XX P-P5DB; ABH83810.
XX
XX Phytase gene sequence and application in yeast thereof.
XX
XX Disclosure; Fig 1; 48pp; Chinese.
XX
XX The invention relates to a coded phytase gene sequence suitable for
XX secretion and expression in yeast and its application. It is mainly
XX characterised by removing nucleotide sequence of +45--+146 bit from phyA
XX total length structure gene sequence, removing Aspergillus niger signal
XX peptide coded sequence of +1--+44 and +147--+159, connecting a part of
XX signal peptide code sequence suitable for secretion and expression at 5',
XX end and connecting a restriction endonuclease site at 3' end. The
XX different carriers can be connected into said gene sequence so as to form
XX a recombinant plasmid with different functions and after the recombinant
XX plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
XX yeast, finally the invented Pasteur Pichia yeast engineering bacterium
XX (CCTCC NO:M200005) can be obtained through the screening process. By
XX using the invention the industrial process of phytase bio-expression can
XX be successfully implemented. The present sequence is that of a
XX polynucleotide of the invention
XX
XX Sequence 1506 BP; 318 A; 465 C; 369 G; 354 T; 0 U; 0 Other;
XX
XX Query Match 99.8%; Score 1347; DB 6; Length 1506;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA 63
Db 160 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA 219

QY 64 TGCTTCTCCGAGACTTCCGATCTTTGGGGTCAATACGACACCGTTCTTCTCTGCAAC 123
Db 220 TGCTTCTCCGAGACTTCCGATCTTTGGGGTCAATACGACACCGTTCTTCTCTGCAAC 279

QY 124 GAATCGTCTATCCCTCGAGTGCCTCGGATCAGAGTCACTTTGGCTCAGTCTC 183
Db 280 GAATCGTCTATCCCTCGAGTGCCTCGGATCAGAGTCACTTTGGCTCAGTCTC 339

QY 184 TCCGTCATGAGCGGTATCCGACCGACTCCGAGCAAGAAATCTCCGCTCTCAT 243
Db 340 TCCGTCATGAGCGGTATCCGACCGACTCCGAGCAAGAAATCTCCGCTCTCAT 399

QY 244 GAGGATCCAGCAGAACCGGACCACTTTGACGGAATAATGCTTCTCTGAAGCATAC 303
Db 400 GAGGATCCAGCAGAACCGGACCACTTTGACGGAATAATGCTTCTCTGAAGCATAC 459

QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGGAGTCTAGTCAACTCC 363
Db 460 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGGAGTCTAGTCAACTCC 519

QY 364 GGCATCAAGTTCTACAGGGGTACGAATCGCTCACAAGGACATCGTTCCATTTCATCCGA 423
Db 520 GGCATCAAGTTCTACAGGGGTACGAATCGCTCACAAGGACATCGTTCCATTTCATCCGA 579

QY 424 TCCTCTGGCTCCAGCGGGTGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCAGAGC 483
Db 580 TCCTCTGGCTCCAGCGGGTGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCAGAGC 639

QY 484 ACAGAGTGAAGATCTCTGTGCCAGCGCGCAATCGTCCGCCAAGATCGAGTGTGTC 543
Db 640 ACAGAGTGAAGATCTCTGTGCCAGCGCGCAATCGTCCGCCAAGATCGAGTGTGTC 699

QY 544 ATTTCGAGGCCAGCTCATCCAAACAACTCTCGAGCCAGGCACTGCTGCTCTTCGAA 603
Db 700 ATTTCGAGGCCAGCTCATCCAAACAACTCTCGAGCCAGGCACTGCTGCTCTTCGAA 759

QY 604 GACAGCAATTCGCGGATACCGTCAAGCCAAATTTTCACCGCCACGTTTCTGCTCCATT 663
Db 760 GACAGCAATTCGCGGATACCGTCAAGCCAAATTTTCACCGCCACGTTTCTGCTCCATT 819

QY 664 CGTCAACGTCGAGAACGACCTGTCGGTGTGACTCTCAGACACACAGAGTGCCTAC 723
Db 820 CGTCAACGTCGAGAACGACCTGTCGGTGTGACTCTCAGACACACAGAGTGCCTAC 879

QY 724 CTCATGGACATGTCTCTTCGACACCATCTCCACGACCGTTCGACACCAAGCTGTCC 783
Db 880 CTCATGGACATGTCTCTTCGACACCATCTCCACGACCGTTCGACACCAAGCTGTCC 939

QY 784 CCCTTCTGTGACTGTTTACCCATCAAGATGATCACTGCTCCTCCAGTCTCTGCTTG 843
Db 940 CCCTTCTGTGACTGTTTACCCATCAAGATGATCACTGCTCCTCCAGTCTCTGCTTG 999

QY 844 AAAAAATATTACGGCCATGCTGAGTAAACCGCTTCGGCCGACCCAGGGGCTCGGCTAC 903
Db 1000 AAAAAATATTACGGCCATGCTGAGTAAACCGCTTCGGCCGACCCAGGGGCTCGGCTAC 1059

QY 904 GCTAAGAGCTCATCGCCGCTGACCCATCGCTGTCAGGATGACACAGTTCGAC 963
Db 1060 GCTAAGAGCTCATCGCCGCTGACCCATCGCTGTCAGGATGACACAGTTCGAC 1119

QY 964 CACACTTTGGACTTCGAGCCCGGCTACCTTTTCGCTCAACTCTCTCTAGCGGACTTT 1023
Db 1120 CACACTTTGGACTTCGAGCCCGGCTACCTTTTCGCTCAACTCTCTCTAGCGGACTTT 1179

QY 1024 TCGCATGACACGGCATCATCTCCATTCTCTTTAGTCTGTGATCAACAGGACATGAG 1083

Db 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTCCAGATGACACCAAGTTCCAC 1801
 QY 964 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGATCAACTCTCTCTAGCGGACTTT 1023
 Db 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGATCAACTCTCTCTAGCGGACTTT 1861
 QY 1024 TCGATGACACGGGATCATCTCCATTCTCTTTAGTCTGTACCAAGGCACTAAG 1083
 Db 1862 TCGATGACACGGGATCATCTCCATTCTCTTTAGTCTGTACCAAGGCACTAAG 1921
 QY 1084 CCGCTATCTACACACCGCTGGAGAAATATCACCCAGACAGATGATTTCTGTCTGTG 1143
 Db 1922 CCGCTATCTACACACCGCTGGAGAAATATCACCCAGACAGATGATTTCTGTCTGTG 1981
 QY 1144 ACGGTTCCGTTTGTCTCCGTTTGTACGTCAGATGATGCTACGGCGGACAGAG 1203
 Db 1982 ACGGTTCCGTTTGTCTCCGTTTGTACGTCAGATGATGCTACGGCGGACAGAG 2041
 QY 1204 CCGCTGTCCGTTTGTCTTAATGATCGCGTTGTCCCGCTGCGATGGGTGTCCGGTTGAT 1263
 Db 2042 CCGCTGTCCGTTTGTCTTAATGATCGCGTTGTCCCGCTGCGATGGGTGTCCGGTTGAT 2101
 QY 1264 GCTTTGGGAGATGACCCGGATAGCTTTGTGAGGGGTTGAGCTTGTAGATCTGGG 1323
 Db 2102 GCTTTGGGAGATGACCCGGATAGCTTTGTGAGGGGTTGAGCTTGTAGATCTGGG 2161
 QY 1324 GGTGATTGGCGGAGTGTGCTTAG 1350
 Db 2162 GGTGATTGGCGGAGTGTGCTTAG 2188

RESULT 7

AAQ11174
 ID AAQ11174 standard; DNA; 6756 BP.

AC AAQ11174;

DT 25-MAR-2003 (revised)

DT 31-MAY-1991 (first entry)

XX Sequence, from overlapping clones, encoding chromosomal phytase.

DE Microbial phytase; animal feeds; inositol; inorganic phosphates; ss.

XX Synthetic.

FH Key Location/Qualifiers
 FT CDS 210..1715
 FT /*tag= b

FT intron /product= "chromosomal phytase"
 FT 254..355
 FT /*tag= a

PN EP420358-A.

PD 03-APR-1991.

PF 27-SEP-1990; 90EP-00202565.

PR 27-SEP-1989; 89EP-00202436.

PR 17-AUG-1990; 90EP-00202231.

XX (KONN) GIST-BROCADES NV.

PA (STAM) DSM NV.

XX Van Gorcom RF, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;

PI Luiten RG, Seltien GCM;

XX WPI; 1991-095799/14.

PT DNA encoding phytase - used for recombinant expression for prodn. of
 PT phytase for conversion of phytate to inositol and inorganic phosphate
 PT esp. in animal feed.

XX Disclosure; Page 32; 61pp; English.

XX This sequence is a compilation of the respective sequences of clones pAF
 CC 2-3, pAF 2-6 and pAF 2-7 identified using oligonucleotide probes. The use
 CC of recombinant DNA methods for the enzyme prodn. allows the large
 CC scale prodn. of proteins and peptides having phytase activity. These are
 CC used for the conversion of phytate to inositol and inorganic phosphate
 CC and can be used in industrial processes. The phosphate content of manure
 CC thus can be decreased. See also AAQ1157-73 and AAQ11175. (Updated on 25-
 CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)

SQ Sequence 6756 BP; 1615 A; 1718 C; 1707 G; 1716 T; 0 U; 0 Other;

Query Match 99.8%; Score 1347; DB 2; Length 6756;
 Best Local Similarity 100.0%; Fred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 63
 Db 369 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 428
 QY 64 TGTCTTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCTTCTCTGCAAC 123
 Db 429 TGTCTTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCTTCTCTGCAAC 488
 QY 124 GAATCGGTCTCTCCCTGAGGTGCCCGGATCGAGTCACTTTTCGCTCAGTCTCTC 183
 Db 489 GAATCGGTCTCTCCCTGAGGTGCCCGGATCGAGTCACTTTTCGCTCAGTCTCTC 548
 QY 184 TCCGTCATGAGCGCGGTATCCGACCGACTTCGAAGGCAAGAAATATCTCCGCTCTCAT 243
 Db 549 TCCGTCATGAGCGCGGTATCCGACCGACTTCGAAGGCAAGAAATATCTCCGCTCTCAT 608
 QY 244 GAGGAGATCCAGACGACGACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC 303
 Db 609 GAGGAGATCCAGACGACGACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC 668
 QY 304 AACTACAGTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGAGTCTAGTCAACTCC 363
 Db 669 AACTACAGTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGAGTCTAGTCAACTCC 728
 QY 364 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAGGACATCGTTCCATTCATCGGA 423
 Db 729 GGCATCAAGTTCTACAGCGGTACGAATCGCTCAAGGACATCGTTCCATTCATCGGA 788
 QY 424 TCCTCTGGCTCCAGCGCGGTGATCGCCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 483
 Db 789 TCCTCTGGCTCCAGCGCGGTGATCGCCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 848
 QY 484 ACCAAGCTGAAGGATCTCGTCCAGCGCGGCAATCGTCCCAAGATCGAGTGTGTC 543
 Db 849 ACCAAGCTGAAGGATCTCGTCCAGCGCGGCAATCGTCCCAAGATCGAGTGTGTC 908
 QY 544 ATTTCCGAGGCCAGCTCATCCAAACACTCTCGAGCCAGGCACTGCACTGTCTTCGAA 603
 Db 909 ATTTCCGAGGCCAGCTCATCCAAACACTCTCGAGCCAGGCACTGCACTGTCTTCGAA 968
 QY 604 GACAGGAATTGGCGGATACCGTGAAGCCAAATTTACCGGCAAGTTCGTCCTCCCTCAT 663
 Db 969 GACAGGAATTGGCGGATACCGTGAAGCCAAATTTACCGGCAAGTTCGTCCTCCCTCAT 1028
 QY 664 CGTCAACGTCCTGGAGAACGACTGCGGTGTGACTCTCACAGACACAGAAAGTACCTAC 723
 Db 1029 CGTCAACGTCCTGGAGAACGACTGCGGTGTGACTCTCACAGACACAGAAAGTACCTAC 1088
 QY 724 CTCATGGACATGTCTCTTCGACACCATCTCCACAGACCGTTCGACACCAAGTGTCC 783
 Db 1089 CTCATGGACATGTCTCTTCGACACCATCTCCACAGACCGTTCGACACCAAGTGTCC 1148
 QY 784 CCCTTCTGTGACTGTTTACCCCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 843

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Db 1149 CCCTTCCTGTACCTGTTCCACCATGAGAGATGATGATCAACTACGACTACCTCCAGTCCCTTG 1208
Qy 844 AAAAAGTATTACGGCCATGTTGCAAGTAAACCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 903
Db 1209 AAAAAGTATTACGGCCATGTTGCAAGTAAACCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 1268
Qy 904 GCTAACGAGCTATCGCCCGCTGACCCACTCGCGCTGTCACGATGACACAGTTCACAC 963
Db 1269 GCTAACGAGCTATCGCCCGCTGACCCACTCGCGCTGTCACGATGACACAGTTCACAC 1328
Qy 964 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1329 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1388
Qy 1024 TCGCATGACAAACGGCATCATCCATTCTCTTTAGCTTGTGTACAAACGGCACTAAG 1083
Db 1389 TCGCATGACAAACGGCATCATCCATTCTCTTTAGCTTGTGTACAAACGGCACTAAG 1448
Qy 1084 CCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGATTCGTCTGCTTGG 1143
Db 1449 CCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGATTCGTCTGCTTGG 1508
Qy 1144 ACGTTCGGTTTGGTTCGCGTTTGTAGTCTGAGATGATGAGTGTACGGCGGAGCAGGAG 1203
Db 1509 ACGTTCGGTTTGGTTCGCGTTTGTAGTCTGAGATGATGAGTGTACGGCGGAGCAGGAG 1568
Qy 1204 CCGTGTCTCTGCTGTTGTTAAATGATCGCGTTTCTCCGCTGCATGGGTGTCGGTTGAT 1263
Db 1569 CCGTGTCTCTGCTGTTGTTAAATGATCGCGTTTCTCCGCTGCATGGGTGTCGGTTGAT 1628
Qy 1264 GCTTTGGGGAGATGATACCCGGGATAGTCTTGTAGGGGGTGTAGCTTTGTAGATCTGGG 1323
Db 1629 GCTTTGGGGAGATGATACCCGGGATAGTCTTGTAGGGGGTGTAGCTTTGTAGATCTGGG 1688
Qy 1324 GGTGATTGGGGAGTGTGTTGCTTAG 1350
Db 1689 GGTGATTGGGGAGTGTGTTGCTTAG 1715

RESULT 8
AAT65137
ID AAT65137 standard; cDNA; 6756 BP.
XX
AC AAT65137;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-AUG-1997 (first entry)
XX
DE Aspergillus ficuum phytase genomic DNA.
XX
KW Phytase; phytate; inositol; animal feed; ss.
XX
OS Aspergillus ficuum; NRRL 3135.
XX
FH Key Location/Qualifiers
FT primer_bind /tag= d
FT /note= "oligonucleotide 1"
FT exon 211..253
FT /tag= a
FT intron 254..355
FT /tag= b
FT exon 356..1715
FT /tag= c
FT primer_bind complement(845..865)
FT /tag= f
FT primer_bind /note= "oligonucleotide 3"
FT 1109..1129
FT /tag= e
FT primer_bind /note= "oligonucleotide 2"
FT 1867..1890
FT /tag= g
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FT /note= "oligonucleotide 4"
XX EP779037-A1.
XX 18-JUN-1997.
XX
PF 27-SEP-1990; 96EP-00202943.
XX
PR 27-SEP-1989; 89EP-00202436.
PR 17-AUG-1990; 90EP-00202231.
PR 27-SEP-1990; 90EP-00202565.
XX
PA (KONN ) GIST-BROCADES NV.
PA (STAM ) DSM NV.
XX
PI Van Paridon PA, Veenstra AE, Luiten RGM, Selten GCM;
PI Van Gorcom RF, Van Hartingsveldt W;
XX
DR WPI: 1997-312513/29.
DR P-PSDB; AAW15124.
XX
FT Fungal phytase - releases inorganic phosphate from myoinositol phosphate,
FT useful to prepare animal feed and reduce phytate levels in manure.
PS Example 8; Fig 6; 61pp; English.
XX
CC Genomic DNA (AAT65137) comprises the phytase gene locus of Aspergillus
CC ficum and includes a coding sequence, interrupted by a single intron,
CC for the 467-amino acid enzyme (AAW15124). The DNA sequence was deduced
CC from clones pAF 2-3, pAF 2-6 and pAF 2-7, which were identified in
CC genomic DNA using probes (see also AAT65138-40) based on CNBr peptides
CC (AAW15128-29) of the phytase. PCR primers (AAT65144-47) based on gene
CC sequences were used to amplify a full-length cDNA clone (AAT65136) for
CC the phytase. Characterisation of the phytase gene will allow large-scale
CC prodn. of phytase in transformed host cells for use e.g. in the food and
CC animal feed industries, and for reducing phytate levels in manure.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
CC on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 6756 BP; 1615 A; 1714 C; 1712 G; 1715 T; 0 U; 0 Other;
Query Match 99.8%; Score 1347; DB 2; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGATCGATCGATCGATCGATCGAT 63
Db 369 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGATCGATCGATCGATCGATCGAT 428
Qy 64 TGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC 123
Db 429 TGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGCGCAAC 488
Qy 124 GAATCGGTTCATCTCCCTGAGTGCCTCGGATCGGATCGAGTCACTTCGCTCAGTCTCTC 183
Db 489 GAATCGGTTCATCTCCCTGAGTGCCTCGGATCGGATCGAGTCACTTCGCTCAGTCTCTC 548
Qy 184 TCCCGTATGAGCGCGGTATCCGACCGACTCCAGGCGGAGAAATATCTCGCTCTCAT 243
Db 549 TCCCGTATGAGCGCGGTATCCGACCGACTCCAGGCGGAGAAATATCTCGCTCTCAT 608
Qy 244 GAGGAGATCCAGCAGACGCGACCACTTTGACGGGAAATATGCTTCTCGAAGACATAC 303
Db 609 GAGGAGATCCAGCAGACGCGACCACTTTGACGGGAAATATGCTTCTCGAAGACATAC 668
Qy 304 AACTACAGTTGGGTGCGAGTGAATCTGCTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 363
Db 669 AACTACAGTTGGGTGCGAGTGAATCTGCTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 728
Qy 364 GGCATCAAGTTCTTACCAGCGGTACGAATCGCTCAAGGAGACATCGTTCCATTCATCCGA 423
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729 GGATCAAGTGTCTACGAGCGGTACGAATCGTCTCAAGAGAACATCGTTTCCATTCATCCGA 788
424 TCCTCTGCTCTCAGCGCGGTGATCGCTCCGCGCAAGAAATTCATCGAGGGGTTCAGAGC 483
789 TCCTCTGCTCTCAGCGCGGTGATCGCTCCGCGCAAGAAATTCATCGAGGGGTTCAGAGC 848
484 ACCAAGCTGAAGATCTCTGCTGCGCGCGCAATGCTGCGCGCAAGATGCGAGTGGTC 543
849 ACCAAGCTGAAGATCTCTGCTGCGCGCGCAATGCTGCGCGCAAGATGCGAGTGGTC 908
544 ATTTCCGAGGCGAGCTCATCAAGCAACTCTCGACCCAGGCACTGCACTGTCTTCCAA 603
909 ATTTCCGAGGCGAGCTCATCAAGCAACTCTCGACCCAGGCACTGCACTGTCTTCCAA 968
604 GACAGCGAATTGGCGGATACCGTTCGAGCCAAATTCACCGCCACGTTGCTCCCTCCATT 663
969 GACAGCGAATTGGCGGATACCGTTCGAGCCAAATTCACCGCCACGTTGCTCCCTCCATT 1028
664 CGTCAACGCTGGAGACGAGCTGTCGCGGTGACTCTCAAGACACAGAGTACCTAC 723
1029 CGTCAACGCTGGAGACGAGCTGTCGCGGTGACTCTCAAGACACAGAGTACCTAC 1088
724 CTCATGACATGTGCTCTCTCGACACCATCTCCACGACCGGTGCGACACCAAGCTGCC 783
1089 CTCATGACATGTGCTCTCTCGACACCATCTCCACGACCGGTGCGACACCAAGCTGCC 1148
784 CCCTTCTGTGACTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCTTGG 843
1149 CCCTTCTGTGACTGTTCAACCATGACGAATGGATCACTACGACTACCTCCAGTCTTGG 1208
844 AAAAGATATTACGGCCATGCTGACGATTAACCGCTCGCGCCGACCCAGGGGTTCGGTAC 903
1209 AAAAGATATTACGGCCATGCTGACGATTAACCGCTCGCGCCGACCCAGGGGTTCGGTAC 1268
904 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTGACGATGACACGAGTTCACAC 963
1269 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTGACGATGACACGAGTTCACAC 1328
964 CACACTTTGGACTGAGCCGCTGACCTTTCCGCTCAACTCTCTCTACGCGGACTTT 1023
1329 CACACTTTGGACTGAGCCGCTGACCTTTCCGCTCAACTCTCTCTACGCGGACTTT 1388
1024 TCGCATGACACGCGCATCATCTCCATCTCTTTGCTTTAGTGTGTACACGCGACTAAG 1083
1389 TCGCATGACACGCGCATCATCTCCATCTCTTTGCTTTAGTGTGTACACGCGACTAAG 1448
1084 CGCTATCTACACGCGGTGGAGATATACCCAGACAGATGATCTCTGCTGCTTGG 1143
1449 CGCTATCTACACGCGGTGGAGATATACCCAGACAGATGATCTCTGCTGCTTGG 1508
1144 ACGGTTCCGTTTGGCTTTCGCTTTGACGTCGAGATGATGACGAGTGTACGCGGAGCAGAG 1203
1509 ACGGTTCCGTTTGGCTTTCGCTTTGACGTCGAGATGATGACGAGTGTACGCGGAGCAGAG 1568
1204 CGCTGTCGCTGCTCTGTTAATGATCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263
1569 CGCTGTCGCTGCTCTGTTAATGATCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1628
1264 GCTTTGGGAGATGATACCCGCGGATAGCTTTGAGGGGGTTCAGCTTTGCTAGATCTGGG 1323
1629 GCTTTGGGAGATGATACCCGCGGATAGCTTTGAGGGGGTTCAGCTTTGCTAGATCTGGG 1688
1324 GGTGATTTGGGCGAGTGTGTTGCTTAG 1350
1689 GGTGATTTGGGCGAGTGTGTTGCTTAG 1715

RESULT 9
ABX13436
ID ABX13436 standard; DNA; 6756 BP.
XX
AC
XX
XX

04-JUN-2003 (first entry)
Plasmids pAF2-3, pAF2-6, pAF2-7 phytase corresponding to Genbank A19451.
Expression cassette; transgenic; promoter; LOX5; plant; food production;
animal feed; seed; stress resistance; disease resistance; starch content;
lipid content; dormancy; fibre content; pharmaceutical production;
fine chemical production; sterile plant; vitamin; flavouring; perfume;
dye; cotyledon; embryonic tissue; stress factor; LOX; ds.
Arabidopsis thaliana.
Synthetic.
DE10127882-A1.
12-DEC-2002.
11-JUN-2001; 2001DE-01027882.
11-JUN-2001; 2001DE-01027882.
(BADI) BASF PLANT SCI GMBH.
Bischoff F, Feussner I, Loyall LP;
WPI; 2003-279966/28.
Cassette for expressing transgene, useful e.g. in production of
pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
of Arabidopsis, provides cotyledon-specific expression.
Claim 5; Page: 28pp; German.
This invention describes a novel cassette for the transgenic expression
of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
thaliana or deletion variants of the LOX5 promoter which are functionally
linked to the nucleic acid of the invention. The cassette is used to
prepare transgenic organisms, especially plants, for production of foods,
animal feeds, seeds (including those with increased resistance to stress
and disease, altered starch/lipid contents or dormancy, or altered fibre
content), pharmaceuticals (especially antibodies, vaccines, enzymes and
pharmaceutical proteins) and fine chemicals (especially fatty acids, flavourings,
vitamins, amino acids, sugars, (un)saturated fatty acids, flavonoids,
perfumes and dyes), also to produce sterile plants. The LOX5 promoter
provides strong and specific expression in cotyledons and/or other early
embryonic tissue, so can degrade, or protect against, stress factors to
which these tissues are particularly sensitive. Since cotyledons are the
main storage organs of seeds, expressing transgenes in them produces
targeted increases/modifications in nutritional value. Expression in the
cotyledons is homogeneous, there are no side effects on other plant
organs (pollen) and the promoter is functional in a wide variety of
plants (ornamentals or crops). This sequence represents a nucleic acid
sequence associated with the Arabidopsis thaliana LOX gene described in
the disclosure of the invention
Sequence 6756 BP; 1635 A; 1712 C; 1712 G; 1714 T; 0 U; 3 Other;
Query Match 99.8%; Score 1347; DB 8; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACCGTTCGATCAGGGGTATCAA 63
Db 369 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACCGTTCGATCAGGGGTATCAA 428
QY 64 TGCTTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACCGCTTCTTCTCTGCAAC 123
Db 429 TGCTTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACCGCTTCTTCTCTGCAAC 488
QY 124 GAATCGGTATCTCCCTGAGGTGCCCGCGGATCGAGTCACTTTGCTCAGTCTCTC 183
Db 489 GAATCGGTATCTCCCTGAGGTGCCCGCGGATCGAGTCACTTTGCTCAGTCTCTC 548

Qy	184	TCCCGTCATGGAGCGGGGTATCCGATCCGACTCCAGGGCAAGAAATACTCCGCTCTCATTT	243
Db	549	TCCCGTCATGGAGCGGGGTATCCGATCCGACTCCAGGGCAAGAAATACTCCGCTCTCATTT	608
Qy	244	GAGGAGATCCAGCAGAACGCGACCACTTTGACGGHAAATATGCTTCTTGAAGACATAC	303
Db	609	GAGGAGATCCAGCAGAACGCGACCACTTTGACGGHAAATATGCTTCTTGAAGACATAC	668
Qy	304	AACATAAGCTTGGGTGCAGATGACTGATCCCTTCGGHAGAACAGAGCTAGTCAACTCC	363
Db	669	AACATAAGCTTGGGTGCAGATGACTGATCCCTTCGGHAGAACAGAGCTAGTCAACTCC	728
Qy	364	GGCATCAAGTTTACACAGCGGTACGAATCGCTCACAGGAAATCTGTTCCATTCATCCGA	423
Db	729	GGCATCAAGTTTACACAGCGGTACGAATCGCTCACAGGAAATCTGTTCCATTCATCCGA	788
Qy	424	TCTCTGGTTCACAGCCGCGTATGCGCTTCGGCAAGAAATTCATCAGAGGCTTCAGAGC	483
Db	789	TCTCTGGTTCACAGCCGCGTATGCGCTTCGGCAAGAAATTCATCAGAGGCTTCAGAGC	848
Qy	484	ACCAAGCTGAAGATCTCTGTGCGCCAGCGCGCAATCGTGGCCCAAGATCGACGTGGTC	543
Db	849	ACCAAGCTGAAGATCTCTGTGCGCCAGCGCGCAATCGTGGCCCAAGATCGACGTGGTC	908
Qy	544	ATTTCCGAGCCAGCTCATCAAACAACACTCTCGACCCAGGCACCTGCATGPTTTCGAA	603
Db	909	ATTTCCGAGCCAGCTCATCAAACAACACTCTCGACCCAGGCACCTGCATGPTTTCGAA	968
Qy	604	GACAGGAATTTGGCGGATACCGTTCGAAGCAAATTCACCGCCAGCTTCGTCGCCCTCCATT	663
Db	969	GACAGGAATTTGGCGGATACCGTTCGAAGCAAATTCACCGCCAGCTTCGTCGCCCTCCATT	1028
Qy	664	CGTCAACGCTCGGAGAACGACCTGTCCGGTGTGACTCTCAACAGACACAGAAGTGACCTAC	723
Db	1029	CGTCAACGCTCGGAGAACGACCTGTCCGGTGTGACTCTCAACAGACACAGAAGTGACCTAC	1088
Qy	724	CTCATGAACATGTGCTCCTTCGACACAACATCTCACACAGACCGTTCGACACCAAGCTGTCC	783
Db	1089	CTCATGAACATGTGCTCCTTCGACACACATCTCACACAGACCGTTCGACACCAAGCTGTCC	1148
Qy	784	CCCTTCGTGACCTGTTTACCCATGACGAATGATCAACTACGACTACCTTCCAGTCTCTTG	843
Db	1149	CCCTTCGTGACCTGTTTACCCATGACGAATGATCAACTACGACTACCTTCCAGTCTCTTG	1208
Qy	844	AAAAAGTATTACCGCCATGTGTGAGGTAAACCCGCTGGCCCGACCCAGGGCGTCGGGTAC	903
Db	1209	AAAAAGTATTACCGCCATGTGTGAGGTAAACCCGCTGGCCCGACCCAGGGCGTCGGGTAC	1268
Qy	904	GCTAACGAGCTCATCGCGGTCTGACCCACTCGCTGTCCACGATGACACGAGTCCAAC	963
Db	1269	GCTAACGAGCTCATCGCGGTCTGACCCACTCGCTGTCCACGATGACACGAGTCCAAC	1328
Qy	964	CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT	1023
Db	1329	CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT	1388
Qy	1024	TCGCATGACAAAGGCATCATCTCATTTCTTTGCTTTAGTCTGTGACACGCACTTAAG	1083
Db	1389	TCGCATGACAAAGGCATCATCTCATTTCTTTGCTTTAGTCTGTGACACGCACTTAAG	1448
Qy	1084	CCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGGATTCTCGTCTGCTTGG	1143
Db	1449	CCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGGATTCTCGTCTGCTTGG	1508
Qy	1144	ACGGTTCGGTTGTTTCGGCTTTGTACGTTCGAGATGATGACGTGTACGGCGGACGAGG	1203
Db	1509	ACGGTTCGGTTGTTTCGGCTTTGTACGTTCGAGATGATGACGTGTACGGCGGACGAGG	1568
Qy	1204	CCGCTGCTCGGTGCTTGGTTTAATGATGTCGGCTGTCTCCGCTGCAATGGTGTCCGGTTGAT	1263
Db	1569	CCGCTGCTCGGTGCTTGGTTTAATGATGTCGGCTGTCTCCGCTGCAATGGTGTCCGGTTGAT	1628
Qy	1264	GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG	1323

Db	1629	GCITTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG	1688
Qy	1324	GCTGATGGCGCGAGTCTTTTGCTTAG	1350
Db	1689	GGTGATGGCGCGAGTCTTTTGCTTAG	1715
RESULT 10			
AAT65136			
ID	AAT65136 standard; cDNA; 1404 BP.		
XX	AC	AAT65136;	
XX	AC	17-OCT-2003 (revised)	
XX	AC	25-MAR-2003 (revised)	
DT	DT	21-AUG-1997 (first entry)	
XX	DE	Aspergillus ficuum phytase cDNA.	
XX	KW	Phytase; phytate; inositol; animal feed; ss.	
XX	OS	Aspergillus ficuum; NRRL 3135.	
XX	FH	Key	Location/Qualifiers
FT	FT	sig_peptide	1..69
FT	FT	mat_peptide	/*tag= a
FT	FT		70..1401
FT	FT		/*tag= b
XX	FN	EP779037-A1.	
XX	PD	18-JUN-1997.	
XX	PF	27-SEP-1990;	96EP-00202943.
XX	PR	27-SEP-1989;	89EP-00202436.
PR	PR	17-AUG-1990;	90EP-00202231.
PR	PR	27-SEP-1990;	90EP-00202565.
XX	XX	(KONN)	GIST-BROCADES NV.
PA	PA	(STAM)	DSM NV.
XX	PI	Van Paridon PA,	Veenstra AE, Luiten RGM, Salten GCM;
PI	PI	Van Gorcom RFW,	Van Hartingsveldt W;
XX	XX	WPI;	1997-312513/29.
XX	DR	P-FSDB;	AAW15124.
PT	PT	Fungal phytase - releases inorganic phosphate from myoinositol phosphate,	
PT	PT	useful to prepare animal feed and reduce phytate levels in manure.	
XX	XX	Claim 1;	Fig 8; 6lpp; English.
XX	XX	A cDNA clone (AAT65136) codes for Aspergillus ficuum phytase (AAW15124),	
CC	CC	an enzyme that catalyses the conversion of phytate to inositol and	
CC	CC	inorganic phosphate. It was obtd. by PCR amplification of A. ficuum	
CC	CC	mRNA/cDNA hybrids using primers (see also AAT65144-47) based on a genomic	
CC	CC	phytase sequence (see also AAT65137). Isolation of this cDNA clone allows	
CC	CC	large-scale prodn. of recombinant phytase in transformed host cells for	
CC	CC	use e.g. in the food and animal feed industries, and for reducing phytate	
CC	CC	levels in animal manure. (Updated on 25-MAR-2003 to correct PF field.)	
CC	CC	(Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to	
CC	CC	correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated	
CC	CC	on 17-OCT-2003 to standardise OS field)	
XX	XX	Sequence	1404 BP; 293 A; 437 G; 343 G; 331 T; 0 U; 0 Other;
XX	XX	Best Local Similarity	99.7%; Score 1345.4; DB 2; Length 1404;
XX	XX	Matches 1346;	Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy	4	CTGGCAGTCCCGCCTCAGAAATCAATCCAGTTCGATACGGTCGATCAGGGGTATCAA	63

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Db      58  CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTCGGATACGGTCGATCAGGGGTATCAA 117
QY      64  TCGTTCTCGAGACTTCGATCTTTGGGGTCAATACGACACGGTTCCTCTCTCTCGCAAC 123
Db      118  TCGTTCTCGAGACTTCGATCTTTGGGGTCAATACGACACGGTTCCTCTCTCTCGCAAC 177
QY      124  GAATCGGTCAATCTCCCTGAGGTGCGCCCGGATGCGAGTCACTTTGCTCAGGTCTC 183
Db      178  GAATCGGTCAATCTCCCTGAGGTGCGCCCGGATGCGAGTCACTTTGCTCAGGTCTC 237
QY      184  TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCAT 243
Db      238  TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCAT 297
QY      244  GAGGAGATCCAGCAACCGGACCACTTTGACGGAATAATGCTTCTCGAAGACATAC 303
Db      298  GAGGAGATCCAGCAACCGGACCACTTTGACGGAATAATGCTTCTCGAAGACATAC 357
QY      304  AACTACAGTTCGGGTGAGATGACTGCTCTCCCTTCGAGAACAGGAGTAGTCAACTCC 363
Db      358  AACTACAGTTCGGGTGAGATGACTGCTCTCCCTTCGAGAACAGGAGTAGTCAACTCC 417
QY      364  GGCATCAAGTTCATACAGCGGTACGAATCGTCTCAAGGAACATCGTTCATTCATCCGA 423
Db      418  GGCATCAAGTTCATACAGCGGTACGAATCGTCTCAAGGAACATCGTTCATTCATCCGA 477
QY      424  TCCCTGCTCAGCGCGGTATCGCTCCGCGAAGAAATTCATCGAGGGCTTCCAGAC 483
Db      478  TCCCTGCTCAGCGCGGTATCGCTCCGCGAAGAAATTCATCGAGGGCTTCCAGAC 537
QY      484  ACCAAGCTGAAGTTCCTCGTCCAGCCCGGCCAATCGTCCGCCAAGATCGACGTGTC 543
Db      538  ACCAAGCTGAAGTTCCTCGTCCAGCCCGGCCAATCGTCCGCCAAGATCGACGTGTC 597
QY      544  ATTTCCGAGGCGAGTATCAACAAACACTCTCGACCCAGGACCTGCTGCTTCGAA 603
Db      598  ATTTCCGAGGCGAGTATCAACAAACACTCTCGACCCAGGACCTGCTGCTTCGAA 657
QY      604  GACAGCAATTCGCGGTATCCGTCGAGCAATTCACCGCCACGTTTCGTCCTCCATT 663
Db      658  GACAGCAATTCGCGGTATCCGTCGAGCAATTCACCGCCACGTTTCGTCCTCCATT 717
QY      664  CGTCAAGCTGAGAGACGACTCTCGGTGTGACTCTCAAGACAGAAAGTGACCTAC 723
Db      718  CGTCAAGCTGAGAGACGACTCTCGGTGTGACTCTCAAGACAGAAAGTGACCTAC 777
QY      724  CTCATGACATGTCTCTTCGACACCATCTCCACAGACCGTTCGACACCAAGCTGTCC 783
Db      778  CTCATGACATGTCTCTTCGACACCATCTCCACAGACCGTTCGACACCAAGCTGTCC 837
QY      784  CCCTTCTGTGACTGTTCACCCATGACGAATGATCACTACGACTACCTCCAGTCTCTG 843
Db      838  CCCTTCTGTGACTGTTCACCCATGACGAATGATCACTACGACTACCTCCAGTCTCTG 897
QY      844  AAAAGTATTACGCCATGTGAGGTAAACCGTCCGCCCGACCCAGGCGTCCGCTAC 903
Db      898  AAAAGTATTACGCCATGTGAGGTAAACCGTCCGCCCGACCCAGGCGTCCGCTAC 957
QY      904  GCTAACGAGTCTATCGCCGCTCTGACCCACTCGCTCTGTCACGATGACACCAAGTCCAA 963
Db      958  GCTAACGAGTCTATCGCCGCTCTGACCCACTCGCTCTGTCACGATGACACCAAGTCCAA 1017
QY      964  CACACTTGTGACTGAGCCCGGTACTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
Db      1018  CACACTTGTGACTGAGCCCGGTACTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1077
QY      1024  TCGCATGACAAACGGCATCATCTCATCTCTTTTGTAGTCTGTACACCGCATTAAG 1083
Db      1078  TCGCATGACAAACGGCATCATCTCATCTCTTTTGTAGTCTGTACACCGCATTAAG 1137
QY      1084  CCGCTATCTACAGGCGGTGGAGATATACCCAGACAGATGAGTCTCGTCTGCTGG 1143

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Db      1138  CCCTATCTATCAACGACCGTGGAGAAATATCAACCAGACAGATGGAATCTCTGTCCTGG 1197
QY      1144  ACGTTTCCTGTTTCTCGGTTTACGTCGAGATGATGACAGTGTACGCGGAGCAGGAG 1203
Db      1198  ACGTTTCCTGTTTCTCGGTTTACGTCGAGATGATGACAGTGTACGCGGAGCAGGAG 1257
QY      1204  CCGTGGTCCGTTCTTGGTTAATGATCCGTTGTCGCCCTGCATGCGGTGTCGTTGAT 1263
Db      1258  CCGTGGTCCGTTCTTGGTTAATGATCCGTTGTCGCCCTGCATGCGGTGTCGTTGAT 1317
QY      1264  GCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1323
Db      1318  GCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1377
QY      1324  GGTGATTTGGCGGAGTGTCTTTGCTTAG 1350
Db      1378  GGTGATTTGGCGGAGTGTCTTTGCTTAG 1404

RESULT 11
ADL91263
ID   ADL91263 standard; DNA; 2665 BP.
XX
AC   ADL91263;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Mutant phytase, E228K, coding sequence, SEQ ID 23.
XX
KW   Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
KW   inositol phosphate; gene; ds.
XX
OS   Aspergillus niger.
OS   Synthetic.
XX
PN   WO2004024895-A2.
XX
XX   25-MAR-2004.
XX
XX   15-SEP-2003; 2003WO-US028923.
XX
XX   13-SEP-2002; 2002US-0410736P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Lei X, Mullaney EJ, Ullah AHJ;
XX
DR   WPI: 2004-270029/25.
XX   P-PSDB; ADL91264.
XX
PT   Novel isolated mutant phytase e.g. PhYA useful for feeding monogastric
PT   animals, improving nutritional value of foodstuffs consumed by animal, in
PT   vitro hydrolysis of phytate or improving nutritional value of foodstuffs
PT   consumed by humans.
XX
XX   Claim 5; SEQ ID NO 23; 215pp; English.
XX
CC   The present invention relates to mutant phytases (I) and their coding
CC   sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC   (I) have altered pH profiles and altered pH optima compared to a
CC   corresponding non-mutant phytase. (I) are useful for improving the
CC   nutritional value of a foodstuff which involves providing a foodstuff
CC   comprising myo-inositol hexakisphosphate, providing (I) and feeding to
CC   the animal the foodstuff in combination with (I) under conditions
CC   effective to increase the bioavailability of phosphate from phytate. (I)
CC   are also useful for feeding a monogastric animal (e.g., fowl species,
CC   porcine species, aquatic species, domestic animal chosen from canine
CC   species and a feline species, or mammalian species) which involves feeding
CC   Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC   foodstuff in combination with (I), to the animal. (I) are also useful for
CC   producing specific inositol phosphate metabolites or products for
CC   nutritional and biomedical applications. The present sequence is the

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CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species) which involves feeding
 CC *Oryctolagus*, *Capra*, a *Bos*, *Equus* and *Ovis* species) chosen from
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is the
 CC coding sequence for one such mutant phytase.
 XX
 SQ

Query Match 99.7%; Score 1345.4; DB 12; Length 2665;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCCGATCAGGGGTATCAA 63
 Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGGTATCAA 901
 QY 64 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCCTCTCTGCGAAAC 123
 Db 902 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCCTCTCTGCGAAAC 961
 QY 124 GAATCGGTCACTCTCCCTGAGGTGCCCGCGGATGCGAGATCACTTTGCGTCAAGTCCCTC 183
 Db 962 GAATCGGTCACTCTCCCTGAGGTGCCCGCGGATGCGAGATCACTTTGCGTCAAGTCCCTC 1021
 QY 184 TCCGCTCATGAGCGCGGTATCCGACCGACTCCAAAGGCGAAGAAATCTCCGCTTCATT 243
 Db 1022 TCCGCTCATGAGCGCGGTATCCGACCGACTCCAAAGGCGAAGAAATCTCCGCTTCATT 1081
 QY 244 GAGGAGATCCAGCAGACGCGACCACTTTGACGGAAATATGCTTCCTGGAAGACATAC 303
 Db 1082 GAGGAGATCCAGCAGACGCGACCACTTTGACGGAAATATGCTTCCTGGAAGACATAC 1141
 QY 304 AACTACAGTTGGTGCAGATGACTGACTCCCTTCGAGAACAGGAGTAGTCAACTCC 363
 Db 1142 AACTACAGTTGGTGCAGATGACTGACTCCCTTCGAGAACAGGAGTAGTCAACTCC 1201
 QY 364 GGCATCAAGTTCTACGACGGTACGATCCGTACAGGAGACATCGTTCATTTCATCCGA 423
 Db 1202 GGCATCAAGTTCTACGACGGTACGATCCGTACAGGAGACATCGTTCATTTCATCCGA 1261
 QY 424 TCCTCTGGCTCCAGCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCCAGAGC 483
 Db 1262 TCCTCTGGCTCCAGCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGCTTCCAGAGC 1321
 QY 484 ACCAGCTGAGGATCTCGTGGCCAGCCCGCGCAATCGTCCGCGAAGATCGACGTGGTC 543
 Db 1322 ACCAGCTGAGGATCTCGTGGCCAGCCCGCGCAATCGTCCGCGAAGATCGACGTGGTC 1381
 QY 544 ATTTCCGAGGCGAGCTCATCAACCAACACTCTCGACCCAGGCACTGCTCTTCGAA 603
 Db 1382 ATTTCCGAGGCGAGCTCATCAACCAACACTCTCGACCCAGGCACTGCTCTTCGAA 1441
 QY 604 GACAGCGAATGGCCGATACCGTGGAGCGAATTTCAACCGCCACGTTGCTCCCTCCATT 663
 Db 1442 GACAGCGAATGGCCGATACCGTGGAGCGAATTTCAACCGCCACGTTGCTCCCTCCATT 1501
 QY 664 CGTCAACGCTGAGAGACGACCTGTCGGGTGTCACCTCTCACAGACAGAGTGACCTAC 723
 Db 1502 CGTCAACGCTGAGAGACGACCTGTCGGGTGTCACCTCTCACAGACAGAGTGACCTAC 1561
 QY 724 CTGATGACATGTGCTCTTCGACACATCTCCAGCACCGTTCGACCAAGCTGTCC 783
 Db 1562 CTGATGACATGTGCTCTTCGACACATCTCCAGCACCGTTCGACCAAGCTGTCC 1621
 QY 784 CCCTTCTGACCTGTTTACCCATGACGATGATCACTACGACTACCTCCAGTCCCTG 843
 Db 1622 CCCTTCTGACCTGTTTACCCATGACGATGATCACTACGACTACCTCCAGTCCCTG 1681

QY 844 AAAAGATTATACGGCAATGTCAGGTAAACCCGCTCGGCCGACCCAGGGCGTCCGCTAC 903
 Db 1682 AGAAAGATTATACGGCAATGTCAGGTAAACCCGCTCGGCCGACCCAGGGCGTCCGCTAC 1741
 QY 904 GCTTAACGAGCTCATCGCCGCTCTGACCCACTCGCTGTCACGATGACACAGTTCACAC 963
 Db 1742 GCTTAACGAGCTCATCGCCGCTCTGACCCACTCGCTGTCACGATGACACAGTTCACAC 1801
 QY 964 CACACTTTGGACTCGAGCCGCGCTACTCTTTCGCTCACTCTACTCTCTACGCGACTT 1023
 Db 1802 CACACTTTGGACTCGAGCCGCGCTACTCTTTCGCTCACTCTACTCTCTACGCGACTT 1861
 QY 1024 TCGCATGACAAAGGCAATCATCTCCATCTCTTTGCTTTAGTCTCTACAAAGGCACTAAG 1083
 Db 1862 TCGCATGACAAAGGCAATCATCTCCATCTCTTTGCTTTAGTCTCTACAAAGGCACTAAG 1921
 QY 1084 CCGCTATCTTACCACGACCGTGGAGAAATATCACCAGACAGATGGATTCTCGTCTCTTGG 1143
 Db 1922 CCGCTATCTTACCACGACCGTGGAGAAATATCACCAGACAGATGGATTCTCGTCTCTTGG 1981
 QY 1144 ACGTTTCGGTTTCTGCTTCGGTTTGTACGTCGAGATGTCAGTGTCAAGCGGAGCAGAG 1203
 Db 1982 ACGTTTCGGTTTCTGCTTCGGTTTGTACGTCGAGATGTCAGTGTCAAGCGGAGCAGAG 2041
 QY 1204 CCGCTGGTCCGCTGCTCTGCTTAATGATCGGTTGTCCGCTGTCATGGGTGTCGGTTGAT 1263
 Db 2042 CCGCTGGTCCGCTGCTCTGCTTAATGATCGGTTGTCCGCTGTCATGGGTGTCGGTTGAT 2101
 QY 1264 GTTTGGGAGATGTCACCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
 Db 2102 GTTTGGGAGATGTCACCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
 QY 1324 GTTGATTTGGGCGAGTGTGTTGCTTAG 1350
 Db 2162 GTTGATTTGGGCGAGTGTGTTGCTTAG 2188

RESULT 13

ADL91247

ID ADL91247 standard; DNA; 2665 BP.

AC ADL91247;

XX 17-JUN-2004 (first entry)

DE Mutant phytase, K300B, coding sequence, SEQ ID 7.

KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
 KW inositol phosphate; gene; ds.XX *Aspergillus niger*.

OS Synthetic.

XX WO2004024885-A2.

XX 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US028923.

XX 13-SEP-2002; 2002US-0410736P.

XX (CORR) CORNELL RES FOUND INC.

XX (USDA) US SEC OF AGRIC.

PI Lei X, Mullane EJ, Ullah AHJ;

DR WPI; 2004-270029/25.

DR P-PSDB; ADL91248.

XX Novel isolated mutant phytase e.g. *PhyA* useful for feeding monogastric
 PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 PT consumed by humans.

XX PS Claim 7; SEQ ID NO 7; 215pp; English.

XX CC The present invention relates to mutant phytases (I) and their coding sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).

CC (I) have altered pH profiles and altered pH optima compared to a corresponding non-mutant phytase. (I) are useful for improving the nutritional value of a feedstuff which involves providing a feedstuff comprising myo-inositol hexakisphosphate, providing (I) and feeding to the animal the feedstuff in combination with (I) under conditions effective to increase the bioavailability of phosphate from phytate. (I) are also useful for feeding a monogastric animal (e.g., fowl species, porcine species, aquatic species, domestic animal chosen from canines, species and a feline species, or mammalian species) which involves feeding Oryctolopus, Capra, a Bos, Equus and Ovis species) chosen from feedstuff in combination with (I), to the animal. (I) are also useful for producing specific inositol phosphate metabolites or products for nutritional and biomedical applications. The present sequence is the coding sequence for one such mutant phytase.

XX SQ Sequence 2665 BP; 632 A; 808 C; 575 G; 650 T; 0 U; 0 Other;

Query Match 99.78; Score 1345.4; DB 12; Length 2665;
Best Local Similarity 99.94; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 63
DB 842 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 901

QY 64 TGGTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACACCGTTCTCTCTCTGGCAAC 123
DB 902 TGGTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGACACCGTTCTCTCTCTGGCAAC 961

QY 124 GAATCGGTGATCTCCCTGAGGTGCGCGCGGATGAGAGTCACTTTCGGTCAAGTCCCTC 183
DB 962 GAATCGGTGATCTCCCTGAGGTGCGCGCGGATGAGAGTCACTTTCGGTCAAGTCCCTC 1021

QY 184 TCCCGTCAAGCGCGGTATCCGACCGACTCCGAGGCAAGAAATCACTCCGTCTCAAT 243
DB 1022 TCCCGTCAAGCGCGGTATCCGACCGACTCCGAGGCAAGAAATCACTCCGTCTCAAT 1081

QY 244 GAGGAGATCCGAGAGCGGACCACTTTGAGGAAATATGCTTCCGTGAGAGATAC 303
DB 1082 GAGGAGATCCGAGAGCGGACCACTTTGAGGAAATATGCTTCCGTGAGAGATAC 1141

QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGAGTGTCACTCC 363
DB 1142 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGAGTGTCACTCC 1201

QY 364 GGCATCAAGTTCTACCGAGGTAGCAATCGGTCAAGGAACATCGTTCCATTCATCCGA 423
DB 1202 GGCATCAAGTTCTACCGAGGTAGCAATCGGTCAAGGAACATCGTTCCATTCATCCGA 1261

QY 424 TCCTCTGCTCCAGCGGTGATCGCTCCGGCAAGAAATCACTCGAGGGGCTTCGAGC 483
DB 1262 TCCTCTGCTCCAGCGGTGATCGCTCCGGCAAGAAATCACTCGAGGGGCTTCGAGC 1321

QY 484 ACCAAGTGAAGGATCTCTGTCGCCAGCCCGGCAATGCTGCCCAAGATCGAGTGGTC 543
DB 1322 ACCAAGTGAAGGATCTCTGTCGCCAGCCCGGCAATGCTGCCCAAGATCGAGTGGTC 1381

QY 544 ATTTCCGAGGCGAGTCTATCAACACACTCTCGACCCAGGACCTGCACCTGCTTCGAA 603
DB 1382 ATTTCCGAGGCGAGTCTATCAACACACTCTCGACCCAGGACCTGCACCTGCTTCGAA 1441

QY 604 GACAGCAATTTGGCGATACCGTGAAGCCCAATTTACCGCCACCGTTCCTCCCAT 663
DB 1442 GACAGCAATTTGGCGATACCGTGAAGCCCAATTTACCGCCACCGTTCCTCCCAT 1501

QY 664 CGTCAACGTCTGGAGAACGACTGTCCTCGGTGTGACTCTCAGACACAGAGTGCACCTAC 723
DB 1502 CGTCAACGTCTGGAGAACGACTGTCCTCGGTGTGACTCTCAGACACAGAGTGCACCTAC 1561

QY 724 CTCATGGACATGTGCTCCTTCGACACCAATCTCCACGACACCGTCGACACCAAGCTGTCC 783
DB 1562 CTCATGGACATGTGCTCCTTCGACACCAATCTCCACGACACCGTCGACACCAAGCTGTCC 1621

QY 784 CCCTTCTGTGACCTGTTCACCCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 843
DB 1622 CCCTTCTGTGACCTGTTCACCCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 1681

QY 844 AAAAGATATTACGGCATGTGTCAGGTAACCCGCTCGGCGCCGACCCAGGGGCTGGCTAC 903
DB 1682 GAAAAGTATTACGGCATGTGTCAGGTAACCCGCTCGGCGCCGACCCAGGGGCTGGCTAC 1741

QY 904 GCTAACGAGCTCATCGCCGCTGTGACCCACCTCGGCTGTCCAGATGACACAGTTCACAC 963
DB 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACCTCGGCTGTCCAGATGACACAGTTCACAC 1801

QY 964 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1023
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QY 1024 TCGCATGACACGCGCATCATCTCCATTTCTTTGTTAGTCTGTGTACACGCGCACTAAG 1083
DB 1862 TCGCATGACACGCGCATCATCTCCATTTCTTTGTTAGTCTGTGTACACGCGCACTAAG 1921

QY 1084 CCGCTATCTACACGACCGTGGAGATATCACCCAGACAGATGGATTCCTCGTCTGCTTGG 1143
DB 1922 CCGCTATCTACACGACCGTGGAGATATCACCCAGACAGATGGATTCCTCGTCTGCTTGG 1981

QY 1144 ACGGTTCCGTTTGTTCGCTTGTACGTCGAGATGATGTCAGTGTGTCAGGCGGAGCAGGAG 1203
DB 1982 ACGGTTCCGTTTGTTCGCTTGTACGTCGAGATGATGTCAGTGTGTCAGGCGGAGCAGGAG 2041

QY 1204 CCGTGGTCCGCTGCTTGGTTAATGATCGGTTGTCCCGCTGTCATGGGTGTCGCTTCAAT 1263
DB 2042 CCGTGGTCCGCTGCTTGGTTAATGATCGGTTGTCCCGCTGTCATGGGTGTCGCTTCAAT 2101

QY 1264 GCTTTGGGAGATGACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
DB 2102 GCTTTGGGAGATGACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161

QY 1324 GGTGATTTGGCGGAGTGTTTTTCCTTAG 1350
DB 2162 GGTGATTTGGCGGAGTGTTTTTCCTTAG 2188

RESULT 14
ADL91251
ID ADL91251 standard; DNA; 2665 BP.
XX AC ADL91251;
XX DT 17-JUN-2004 (first entry)
XX DE Mutant phytase, Q50L, coding sequence, SEQ ID 11.
XX KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
XX KW inositol phosphate; gene; ds.
XX OS Aspergillus niger.
XX OS Synthetic.
XX PN WO2004024885-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US028923.
XX PR 13-SEP-2002; 2002US-0410736P.
XX PA (CORR) CORNELL RES FOUND INC.
XX PA (USDA) US SEC OF AGRIC.

PI Lei X, Mullaney EJ, Ullah AHJ;
 XX WPI: 2004-270029/25.
 DR P-PSDB; ADL91252.
 XX Novel isolated mutant phytase e.g. *PhyA* useful for feeding monogastric
 PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 PT consumed by humans.
 XX
 PS Claim 2; SEQ ID NO 11; 215pp; English.
 XX The present invention relates to mutant phytases (I) and their coding
 CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
 CC (I) have altered pH profiles and altered pH optima compared to a
 CC corresponding non-mutant phytase. (I) are useful for improving the
 CC nutritional value of a foodstuff which involves providing a foodstuff
 CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
 CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC *Oryctolagus*, *Capra*, a *Bos*, *Equus* and *Ovis* species) which involves feeding
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is the
 CC coding sequence for one such mutant phytase.
 XX
 SQ Sequence 2665 BP; 632 A; 808 C; 574 G; 651 T; 0 U; 0 Other;

Query Match 99.7%; Score 1345.4; DB 12; Length 2665;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 63
 DB 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 901
 64 TCGTTCTCCGAGATTCGATCTTTGGGGTCAATACGACCGTTCTTCTCTCGCAAAC 123
 DB 902 TCGTTCTCCGAGATTCGATCTTTGGGGTCAATACGACCGTTCTTCTCTCGCAAAC 961
 124 GAATCGGTCAATCTCCCTGAGTCCCGCGGATGCGAGTCACTTTCGCTCAGGTCTTC 193
 DB 962 GAATCGGTCAATCTCCCTGAGTCCCGCGGATGCGAGTCACTTTCGCTCAGGTCTTC 1021
 184 TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATACCTCCGCTCAAT 243
 DB 1022 TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATACCTCCGCTCAAT 1081
 244 GAGGATCCAGCAGACGCGACCACTTTGACGGAATAATGCTTCTCGAAGACATAC 303
 DB 1082 GAGGATCCAGCAGACGCGACCACTTTGACGGAATAATGCTTCTCGAAGACATAC 1141
 304 AACTACAGCTTGGTGAGATGACTGACTCCCTTCGGAACAGGAGTAGTCAACTCC 363
 DB 1142 AACTACAGCTTGGTGAGATGACTGACTCCCTTCGGAACAGGAGTAGTCAACTCC 1201
 364 GGCAATCAAGTTCTACGAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTCGGA 423
 DB 1202 GGCAATCAAGTTCTACGAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTCGGA 1261
 424 TCCTCTGGCTCCAGCCCGGTGATCGCTCCCGCAAGAAATTCATCGAGGCTTCCAGAGC 483
 DB 1262 TCCTCTGGCTCCAGCCCGGTGATCGCTCCCGCAAGAAATTCATCGAGGCTTCCAGAGC 1321
 484 ACCAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTCGCCAAGATCGACGTGGTC 543
 DB 1322 ACCAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTCGCCAAGATCGACGTGGTC 1381
 544 ATTTCCGAGCCAGCTCATCAACACACTCTCGACCCAGGACCTGCTGCTTCGAA 603

DB 1382 ATTTCCGAGCCAGCTCATCCAAACACACTCTCGACCCAGGACCTGCACTGCTTCGAA 1441
 QY 604 GACAGCAATTTGGCCGATACCGTTCGAAGCAATTTACCGCCACGTTCTGTCCTCCATT 663
 DB 1442 GACAGCAATTTGGCCGATACCGTTCGAAGCAATTTACCGCCACGTTCTGTCCTCCATT 1501
 QY 664 CGTCAACGCTCGAGAACACCTGTCGGGTGACTCTCACAGACACAGAGTGACCTAC 723
 DB 1502 CGTCAACGCTCGAGAACACCTGTCGGGTGACTCTCACAGACACAGAGTGACCTAC 1561
 QY 724 CTCATCGACATGCTCTCTTCGACACACCATCTCCACGACACCGTTCGACCAAGCTGTCC 783
 DB 1562 CTCATCGACATGCTCTCTTCGACACACCATCTCCACGACACCGTTCGACCAAGCTGTCC 1621
 QY 784 CCTCTCTGACTGTTCTACCCCATGACGATGATGATGATGATGATGATGATGATGATG 843
 DB 1622 CCTCTCTGACTGTTCTACCCCATGACGATGATGATGATGATGATGATGATGATGATG 1681
 QY 844 AAAAAGTATTACGGCCATGCTGTCAGGTAAACCGCTCGGCCCGCCAGCCAGGGGTCTAC 903
 DB 1682 AAAAAGTATTACGGCCATGCTGTCAGGTAAACCGCTCGGCCCGCCAGCCAGGGGTCTAC 1741
 QY 904 GCTAACGAGCTATCGCCCGTCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
 DB 1742 GCTAACGAGCTATCGCCCGTCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801
 QY 964 CACACTTTTGGACTTCGAGCCCGGTACTCTTTCGCTCAACTCTTCTCTCTCTCTCTCTCT 1023
 DB 1802 CACACTTTTGGACTTCGAGCCCGGTACTCTTTCGCTCAACTCTTCTCTCTCTCTCTCTCT 1861
 QY 1024 TCGCATGACACGGCATCATCTTCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1083
 DB 1862 TCGCATGACACGGCATCATCTTCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1921
 QY 1084 CCGCTATCTTACCACACCGCTGAGAAATATACCCAGACAGATGATGATGATGATGATGATGATG 1143
 DB 1922 CCGCTATCTTACCACACCGCTGAGAAATATACCCAGACAGATGATGATGATGATGATGATGATG 1981
 QY 1144 ACGGTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1203
 DB 1982 ACGGTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2041
 QY 1204 CCGCTGCTCCGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1263
 DB 2042 CCGCTGCTCCGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2101
 QY 1264 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTCTAGATCTGGG 1323
 DB 2102 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTCTAGATCTGGG 2161
 QY 1324 GGTGATTTGGGGAGTGTGTTGCTTAG 1350
 DB 2162 GGTGATTTGGGGAGTGTGTTGCTTAG 2188

RESULT 15
 ADL91259
 ID ADL91259 standard; DNA; 2665 BP.
 XX
 AC ADL91259;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Mutant phytase, K94E, coding sequence, SEQ ID 19.
 XX
 KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
 XX inositol phosphate; gene; ds.
 OS *Aspergillus niger*.
 OS Synthetic.
 XX
 FN WO2004024885-A2.
 XX

PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US028923.
XX
PR 13-SEP-2002; 2002US-0410736P.
XX
XX (CORR) CORNELL RES FOUND INC.
PA (USDA) US SEC OF AGRIC.
XX
XX
PI Lei X, Mullaney EJ, Ullah AHJ;
XX
XX WPI; 2004-270029/25.
DR
DR P-PSDB; ADL91260.
XX
XX Novel isolated mutant phytase e.g. PhYA useful for feeding monogastric
PT animals, improving nutritional value of feedstuffs consumed by animal, in
PT vitro hydrolysis of phytate or improving nutritional value of feedstuffs
PT consumed by humans.
XX
XX Claim 4; SEQ ID NO 19; 215pp; English.
XX
XX The present invention relates to mutant phytases (I) and their coding
CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC (I) have altered pH profiles and altered pH optima compared to a
CC corresponding non-mutant phytase. (I) are useful for improving the
CC nutritional value of a feedstuff which involves providing a feedstuff
CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
CC the animal the feedstuff in combination with (I) under conditions
CC effective to increase the bioavailability of phosphate from phytate. (I)
CC are also useful for feeding a monogastric animal (e.g., fowl species,
CC porcine species, aquatic species, domestic animal chosen from canine
CC species and a feline species, or mammalian species chosen from
CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC feedstuff in combination with (I), to the animal. (I) are also useful for
CC producing specific inositol phosphate metabolites or products for
CC nutritional and biomedical applications. The present sequence is the
CC coding sequence for one such mutant phytase.
XX
SQ Sequence 2665 BP; 632 A; 808 C; 575 G; 650 T; 0 U; 0 Other;
Query Match 99.7%; Score 1345.4; DB 12; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
4 CTGCGAGTCCCGGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCGGGGTATCAA 63
842 CTGCGAGTCCCGGCTCGAGAAATCAATCCAGTTCGATACGGTCGATCGGGGTATCAA 901
64 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGCACCGTTCTTCTCTCTGGCAAC 123
902 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGCACCGTTCTTCTCTGGCAAC 961
124 GAATCGGTTCATCTCCCTGAGGTGCGCCCGCGATGCAGAGTCACTTTTCGTCAGGTCTC 183
962 GAATCGGTTCATCTCCCTGAGGTGCGCCCGCGATGCAGAGTCACTTTTCGTCAGGTCTC 1021
184 TCCGCTCATGAGCGCGGTATCCGACCGACTCCCAAGGCAAGAAATCTCCGCTCTCATTT 243
1022 TCCGCTCATGAGCGCGGTATCCGACCGACTCCCAAGGCAAGAAATCTCCGCTCTCATTT 1081
244 GAGGAGATCCAGCAGAACCGCACCACTTTTCAACGGAATAATGCTTCTTGAAGACATAC 303
1082 GAGGAGATCCAGCAGAACCGCACCACTTTTGAACGGAATAATGCTTCTTGAAGACATAC 1141
304 AACTACAGTTCGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTACTCACTCC 363
1142 AACTACAGTTCGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTACTCACTCC 1201
364 GGCATCAAGTTCATACACGGGTACGAATCGCTTCAAGGAACATCGTTTCCATTTCATCGA 423
1202 GGCATCAAGTTCATACACGGGTACGAATCGCTTCAAGGAACATCGTTTCCATTTCATCGA 1261
424 TCCTCTGGCTCAGCCGGTGATCGCTTCGGGCAAGAAATTCATCGAGGGCTTCAGAGC 483

1262 TCCTCTGGCTCAGCCGGTGATCGCTTCGGGCAAGAAATTCATCGAGGGGTTCAGAGC 1321
484 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCAATCGTCGCCCAAGATCGAGCTGTC 543
1322 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCAATCGTCGCCCAAGATCGAGCTGTC 1381
544 ATTTCCGAGGCGAGCTCATCAACAACTCTCGACCAGGCACTGTGACTGTCTTCGAA 603
1382 ATTTCCGAGGCGAGCTCATCAACAACTCTCGACCAGGCACTGTGACTGTCTTCGAA 1441
604 GACAGGAATTCGCGGATACCGTTCGAGCCCAATTCACGCCAGTTCGTCCTCCCTCCATT 663
1442 GACAGGAATTCGCGGATACCGTTCGAGCCCAATTCACGCCAGTTCGTCCTCCCTCCATT 1501
664 CGTCAACGCTCTGGAGAACGACCTGTCCGCTGTGACTCTCACAGACACAGAGTACCTAC 723
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724 CTCATGGACATGTGCTCCTTCGACACCACTCTCCACAGCAGCGTGCAGACCAAGCTGCC 783
1562 CTCATGGACATGTGCTCCTTCGACACCACTCTCCACAGCAGCGTGCAGACCAAGCTGCC 1621
784 CCCTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTAGCACTACTCCAGTCTCTG 843
1622 CCCTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTAGCACTACTCCAGTCTCTG 1681
844 AAAAGTATTACGGGCATGTGTGAGTAAACCGCTCGGCCGACCCAGGGGCTCGGCTAC 903
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904 GCTAACGAGCTCATCGCGCTCGACCCACTCGCTGTCCAGATGACACCAAGTTCACAC 963
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964 CACACTTTGGACTCGAGCCCGCTACTTTTCGCTCAACTCTACTCTCTACGCGACTTT 1023
1802 CACACTTTGGACTCGAGCCCGCTACTTTTCGCTCAACTCTACTCTCTACGCGACTTT 1861
1024 TGCATGACACCGGCATCATCTCCATTCTCTTTGCTTTAGTCTGTACAAAGGCACTAAG 1083
1862 TGCATGACACCGGCATCATCTCCATTCTCTTTGCTTTAGTCTGTACAAAGGCACTAAG 1921
1084 CGCTATCTACCAACGCGTGGAGAAATATCACCCAGACAGATGGATTTCTCGTCTGCTGG 1143
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1264 GCTTTGGGAGATGTACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG 1323
2102 GCTTTGGGAGATGTACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
1324 GGTGATTGGCGGAGTGTTCGCTTAG 1350
2162 GGTGATTGGCGGAGTGTTCGCTTAG 2188

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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1347	99.8	1404	3	US-09-233-510-33
6	1347	99.8	6756	1	US-08-151-574-31
7	1347	99.8	6756	2	US-08-419-448-31
8	1347	99.8	6756	3	US-09-233-510-31
9	1275	94.4	2363	1	US-07-923-724-7
10	1275	94.4	2363	2	US-08-609-426A-7
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28 621.4 46.0 1404 4 US-09-684-855-162 Sequence 162, Appl
29 621.4 46.0 1404 4 US-09-488-265B-28 Sequence 28, Appl
30 613.4 45.4 1426 3 US-03-121-425-3 Sequence 3, Appl
31 613.4 45.4 1426 4 US-09-634-493A-3 Sequence 3, Appl
32 613.4 45.4 1426 4 US-09-684-855-117 Sequence 117, Appl
33 613.4 45.4 1426 4 US-09-488-265B-15 Sequence 15, Appl
34 611.8 45.3 1404 4 US-09-488-265B-90 Sequence 90, Appl
35 608.6 45.1 1404 4 US-09-488-265B-92 Sequence 92, Appl
36 608.6 45.1 1426 4 US-09-684-855-140 Sequence 140, Appl
37 608.6 45.1 1426 4 US-09-488-265B-25 Sequence 25, Appl
38 602 44.6 1404 4 US-09-684-855-164 Sequence 164, Appl
39 602 44.6 1404 4 US-09-488-265B-30 Sequence 30, Appl
40 600 44.4 1404 4 US-09-684-855-166 Sequence 166, Appl
41 600 44.4 1404 4 US-09-488-265B-32 Sequence 32, Appl
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43 598.4 44.3 1571 3 US-08-868-435-32 Sequence 32, Appl
44 598.4 44.3 1571 3 US-08-744-231-32 Sequence 32, Appl
45 598.4 44.3 1571 3 US-09-044-718-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-151-574-33
; Sequence 33, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selden
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

; LOCATION: 1..1401									
; FEATURE: mat_peptide									
; NAME/KEY: mat_peptide									
; LOCATION: 70									
; US-08-146-424-19									
Query Match									
Best Local Similarity 99.8%; Score 1347; DB 1; Length 1404;									
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	4	CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA	63						
Db	58	CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA	117						
QY	64	TGCTTCTCCGAGATTGCAATCTTGGGGTCAATACGACCGTTCTTCTCTGCGCAAC	123						
Db	118	TGCTTCTCCGAGATTGCAATCTTGGGGTCAATACGACCGTTCTTCTCTGCGCAAC	177						
QY	124	GAATCGGTATCTCCCTGAGGTGCGCGCGATGAGATGATCTTCCGTCAGGTCTCTC	183						
Db	178	GAATCGGTATCTCCCTGAGGTGCGCGCGATGAGATGATCTTCCGTCAGGTCTCTC	237						
QY	184	TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATATCTCCGCTCTCAT	243						
Db	238	TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATATCTCCGCTCTCAT	297						
QY	244	GAGGAGATCCAGCAAGACCGGACCACTTTGACGGAATATGCTTCTTGAGAGATAC	303						
Db	298	GAGGAGATCCAGCAAGACCGGACCACTTTGACGGAATATGCTTCTTGAGAGATAC	357						
QY	304	AACATACAGTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGGAGTGTAGTCAACTCC	363						
Db	358	AACATACAGTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGGAGTGTAGTCAACTCC	417						
QY	364	GGCATCAAGTTCTACAGCGGTAGCAATCGTCAAGGAACATCGTTCATTCATCCGA	423						
Db	418	GGCATCAAGTTCTACAGCGGTAGCAATCGTCAAGGAACATCGTTCATTCATCCGA	477						
QY	424	TCCTCTGGCTCCAGCGCGTGTGCTCGGCAAGAAATTCATCGAGGGCTTCCAGAGC	483						
Db	478	TCCTCTGGCTCCAGCGCGTGTGCTCGGCAAGAAATTCATCGAGGGCTTCCAGAGC	537						
QY	484	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTGGCCCAAGATCGAGTGGTC	543						
Db	538	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGGCAATCGTGGCCCAAGATCGAGTGGTC	597						
QY	544	ATTTCCGAGGCGAGTATCCAAACACATCTGACCCAGGACCTGCTGCTTCGAA	603						
Db	598	ATTTCCGAGGCGAGTATCCAAACACATCTGACCCAGGACCTGCTGCTTCGAA	657						
QY	604	GACAGCGAATTGGCGGATACCGTCAAGCCCAATTTACCGCCAGTTCGTCCTCCATT	663						
Db	658	GACAGCGAATTGGCGGATACCGTCAAGCCCAATTTACCGCCAGTTCGTCCTCCATT	717						
QY	664	CGTCAACGCTGGAGAACGACCTGTCCGGTGTGATCTTCACAGACACAGAGTACCTAC	723						
Db	718	CGTCAACGCTGGAGAACGACCTGTCCGGTGTGATCTTCACAGACACAGAGTACCTAC	777						
QY	724	CTCATGGACATGTGCTCTTCGACACCATCTCCACGACCGTCCGACCAAGCTGTCC	783						
Db	778	CTCATGGACATGTGCTCTTCGACACCATCTCCACGACCGTCCGACCAAGCTGTCC	837						
QY	784	CCCTTCTGTGACCTGTTCCACCATACGAAATGGATCAACTAGCATCTCTCCAGTCCCTG	843						
Db	838	CCCTTCTGTGACCTGTTCCACCATACGAAATGGATCAACTAGCATCTCTCCAGTCCCTG	897						
QY	844	AAAAAGTATTACGGCATGTGCGAGTAACCGGTCCGCCCGACCCAGGGGTGCGGTAC	903						
Db	898	AAAAAGTATTACGGCATGTGCGAGTAACCGGTCCGCCCGACCCAGGGGTGCGGTAC	957						
QY	904	GCTAACGAGCTCATCGCCCGTCTGACCCCACTCGCTGTCCACGATGACACAGTCCCAAC	963						
Db	958	GCTAACGAGCTCATCGCCCGTCTGACCCCACTCGCTGTCCACGATGACACAGTCCCAAC	1017						

RESULT 3
US-08-693-709-1
; Sequence 1, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN COLUEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKENA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

QY	964	CACACTTTGGACTCGAGCGGGCTACCTTCCGCTCAACTCTACTCTCTCTACGCGACTTT	1023
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QY	1024	TGGATGACAAACGGCATCATCTCCATTTCTTTAGTCTGTGTACAAACGGCACTAAG	1083
Db	1078	TGGATGACAAACGGCATCATCTCCATTTCTTTAGTCTGTGTACAAACGGCACTAAG	1137
QY	1084	CGCTATCTACACACCGGTGGAGATATCACCCAGACAGATGATCTCTCTGCTTGG	1143
Db	1138	CGCTATCTACACACCGGTGGAGATATCACCCAGACAGATGATCTCTCTGCTTGG	1197
QY	1144	ACGGTTCCGTTTGGCTTCCGCTTTGTACGTCCAGATGATGACAGCGGAGCAGGAG	1203
Db	1198	ACGGTTCCGTTTGGCTTCCGCTTTGTACGTCCAGATGATGACAGCGGAGCAGGAG	1257
QY	1204	CGCTGGTCCGTTTGGTAAATGATCGCTTGTCCGCTGCGATGGTGTCCGTTGAT	1263
Db	1258	CGCTGGTCCGTTTGGTAAATGATCGCTTGTCCGCTGCGATGGTGTCCGTTGAT	1317
QY	1264	GCTTTGGGAGATGACCCGGGATAGCTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG	1323
Db	1318	GCTTTGGGAGATGACCCGGGATAGCTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG	1377
QY	1324	GCTGATTGGCGGAGTGTTTGCTTAG	1350
Db	1378	GCTGATTGGCGGAGTGTTTGCTTAG	1404

/ LENGTH: 1404 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / FEATURE:
 / NAME/KEY: Coding Sequence
 / LOCATION: 1...1401
 / OTHER INFORMATION:
 / NAME/KEY: mat_peptide
 / LOCATION: 70...1401
 / OTHER INFORMATION:
 / NAME/KEY: Signal Sequence
 / LOCATION: 1...72
 / OTHER INFORMATION:
 / US-08-693-709-1

Query Match 99.8%; Score 1347; DB 1; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTGCATCAGGGGTATCAA	63
Db	58	CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTGCATCAGGGGTATCAA	117
QY	64	TGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCTTCTCTCTGCGAAAC	123
Db	118	TGCTTCTCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCTTCTCTCTGCGAAAC	177
QY	124	GAATCGGTCAATCTCCCTGAGTGCCTCCCGGATGCGAGTCACTTTGCTCAGGTCTC	183
Db	178	GAATCGGTCAATCTCCCTGAGTGCCTCCCGGATGCGAGTCACTTTGCTCAGGTCTC	237
QY	184	TCCGTCATGAGCGCGGTATCCGACGACTCCAGGCGAAGAAATACCTCGCTCTCAT	243
Db	238	TCCGTCATGAGCGCGGTATCCGACGACTCCAGGCGAAGAAATACCTCGCTCTCAT	297
QY	244	GAGGAGATCCAGCAAGCGACCACTTTGACGGAAATATGCTTCTTGAAGACATAC	303
Db	298	GAGGAGATCCAGCAAGCGACCACTTTGACGGAAATATGCTTCTTGAAGACATAC	357
QY	304	AATACAGCTTGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTAGTCAATCC	363
Db	358	AATACAGCTTGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTAGTCAATCC	417
QY	364	GGCATCAAGTTCTACACGGGTACGATCGCTCAAGGAACATCGTTCCATTATCCGA	423
Db	418	GGCATCAAGTTCTACACGGGTACGATCGCTCAAGGAACATCGTTCCATTATCCGA	477
QY	424	TCCTCTGCTCCAGCGGTGATCGCTTCGGCAAGAAATTCATCGAGGCTTCCAGAGC	483
Db	478	TCCTCTGCTCCAGCGGTGATCGCTTCGGCAAGAAATTCATCGAGGCTTCCAGAGC	537
QY	484	ACCAAGCTGAAGGATCTCTGCGCCAGCGCCCAATCGTCCGCAAGATCGAGTGGTC	543
Db	538	ACCAAGCTGAAGGATCTCTGCGCCAGCGCCCAATCGTCCGCAAGATCGAGTGGTC	597
QY	544	ATTTCCAGGCGCACTATCAACAACACTCTCGACCCAGGCACTGCACTGTTCCGA	603
Db	598	ATTTCCAGGCGCACTATCAACAACACTCTCGACCCAGGCACTGCACTGTTCCGA	657
QY	604	GACAGCAATTTGGCGGTACCGTGCAGCAATTTACCGCGCAAGTTCGTCCTCCATT	663
Db	658	GACAGCAATTTGGCGGTACCGTGCAGCAATTTACCGCGCAAGTTCGTCCTCCATT	717
QY	664	CGTCAACGCTTGGAGACGACCTGCTCGGTGTGACTCTCACAGACAGAAAGTGCCTAC	723
Db	718	CGTCAACGCTTGGAGACGACCTGCTCGGTGTGACTCTCACAGACAGAAAGTGCCTAC	777
QY	724	CTCATGACATGTCTCTTTCGACACCATCTCACAGCAAGCGTTCAGACCAAGTGTCC	783
Db	778	CTCATGACATGTCTCTTTCGACACCATCTCACAGCAAGCGTTCAGACCAAGTGTCC	837
QY	784	CCCTTCTGTGACCTGTTTCAACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTT	843

Db	838	CCCTTCTGTGACCTGTTTCAACCCATGACGAATGATCACTACGACTACCTCCAGTCTT	897
QY	844	AAAAAGTATTACGGCCATGTTGAGTAACCGCTCGGCCACCCAGGGGCTCGGCTAC	903
Db	898	AAAAAGTATTACGGCCATGTTGAGTAACCGCTCGGCCACCCAGGGGCTCGGCTAC	957
QY	904	GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCCCTGTCACGATGACACCACTT	963
Db	958	GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCCCTGTCACGATGACACCACTT	1017
QY	964	CACACTTTGAGCTCGAGCCCGGCTACCTTTCCGCTCACTCTTACCGGACTTT	1023
Db	1018	CACACTTTGAGCTCGAGCCCGGCTACCTTTCCGCTCACTCTTACCGGACTTT	1077
QY	1024	TGCGATGACAAAGGCTATCTCTCCATTTCTTTTGGTCTTGTAGTCTGTACAAAGGCT	1083
Db	1078	TGCGATGACAAAGGCTATCTCTCCATTTCTTTTGGTCTTGTAGTCTGTACAAAGGCT	1137
QY	1084	CCGCTATCTACCAAGCGCTGAGAAATATACCCAGACAGATGGAATCTCTGCTTGG	1143
Db	1138	CCGCTATCTACCAAGCGCTGAGAAATATACCCAGACAGATGGAATCTCTGCTTGG	1197
QY	1144	ACGTTTCCGTTTGGCTTTCGCGTTTGTACGTCGAGATGATGAGTGTACGCGGAGCAG	1203
Db	1198	ACGTTTCCGTTTGGCTTTCGCGTTTGTACGTCGAGATGATGAGTGTACGCGGAGCAG	1257
QY	1204	CCGCTGCTCGTGTCTTGGTTAATGATCGCGTGTTCGCGCTGCATGGGTTCGGTGT	1263
Db	1258	CCGCTGCTCGTGTCTTGGTTAATGATCGCGTGTTCGCGCTGCATGGGTTCGGTGT	1317
QY	1264	GCTTTGGGAGATGTACCCGGGATGACTTTGTGAGGGGTTGAGCTTGTCTAGATCTGG	1323
Db	1318	GCTTTGGGAGATGTACCCGGGATGACTTTGTGAGGGGTTGAGCTTGTCTAGATCTGG	1377
QY	1324	GCTGATTTGGGCGGAGTGTTCCTTAG	1350
Db	1378	GCTGATTTGGGCGGAGTGTTCCTTAG	1404

RESULT 4
 US-08-419-448-33
 ; Sequence 33, Application US/08419448
 ; Patent No. 5863533
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorkom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Seltin
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; TITLE OF INVENTION: Phytase
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006-1888
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/419,448
 ; FILING DATE: 10-APR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus ficum (Aspergillus niger)
STRAIN: NREL 3135
US-08-419-448-33

Query Match 99.8%; Score 1347; DB 2; Length 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGACGTCCTCCGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 63
Db 58 CTGACGTCCTCCGCTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 117
QY 64 TGCTTCTCCGAGACTTCGATCTTTGGGTCAATACGACCGTTCTTCTCTCTGGCAAC 123
Db 118 TGCTTCTCCGAGACTTCGATCTTTGGGTCAATACGACCGTTCTTCTCTCTGGCAAC 177
QY 124 GAATCGGTCTATCTCCCTGAGGTGCCCGCGGATGACAGTCACTTTTCGTCAGGTCCTC 183
Db 178 GAATCGGTCTATCTCCCTGAGGTGCCCGCGGATGACAGTCACTTTTCGTCAGGTCCTC 237
QY 184 TCCGCTCATGAGCGCGGTATCCGACGACTCCAGGGCAAGAAATCTCCGTCCTCAT 243
Db 238 TCCGCTCATGAGCGCGGTATCCGACGACTCCAGGGCAAGAAATCTCCGTCCTCAT 297
QY 244 GAGGAGATCCAGAGAACGCGACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC 303
Db 298 GAGGAGATCCAGAGAACGCGACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC 357
QY 304 AACTACAGTTGGTGCAGATGACCTGACTCCCTTCGGGAAACAGGAGTGTAGTCACTCC 363
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QY 484 ACCAAGTGAAGGATCTCTGTCGCGAGCGCGGCAATCGTCCGCAAGATCGAGTGGTC 543
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QY 724 CTCATGGACATGTGCTCTTCGACACCATCTCCACAGACCGTCCGACCAAGCTGCC 783
Db 778 CTCATGGACATGTGCTCTTCGACACCATCTCCACAGACCGTCCGACCAAGCTGCC 837

QY 784 CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTAGACTACTCTCAGTCTCTG 843
Db 838 CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTAGACTACTCTCAGTCTCTG 897
QY 844 AAAAAAGTATTACGGCCATGTCGAGTAACCCCGTTCGGCCGAGACCCAGGGGCTCGGCTAC 903
Db 898 AAAAAAGTATTACGGCCATGTCGAGTAACCCCGTTCGGCCGAGACCCAGGGGCTCGGCTAC 957
QY 904 GCTAACGAGCTCATCGCCGCTGTGACCCACACCTGCTGTCACGATGACACAGTTCGCAAC 963
Db 958 GCTAACGAGCTCATCGCCGCTGTGACCCACACCTGCTGTCACGATGACACAGTTCGCAAC 1017
QY 964 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
Db 1018 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1077
QY 1024 TCGCATGACACGGCATCATCTCCATTCTCTTTGCTTTAGTCTGTACAAAGGCACTAAG 1083
Db 1078 TCGCATGACACGGCATCATCTCCATTCTCTTTGCTTTAGTCTGTACAAAGGCACTAAG 1137
QY 1084 CGCTATCTACACACCGTGGAGATATCACCCAGACAGATGGATTCTCTGCTGCTTGG 1143
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Db 1198 ACGTTCCGTTTGGCTTCGCGTTTGTACGTCGAGATGATCGAGTGTACGCGGAGCAGAG 1257
QY 1204 CGCTGTCGCTGCTTGGTTAATGATCGGTTGTCGCTGCTGATGGTGTCCGCTTGTAT 1263
Db 1258 CGCTGTCGCTGCTTGGTTAATGATCGGTTGTCGCTGCTGATGGTGTCCGCTTGTAT 1317
QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db 1318 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1377
QY 1324 GGTGATTGGCGGAGTGTTCCTTAG 1350
Db 1378 GGTGATTGGCGGAGTGTTCCTTAG 1404

RESULT 5

US-09-233-510-33
; Sequence 33, Application US/09233510
; Patent No. 6350602
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Anemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,510
; FILING DATE:
; CLASSIFICATION:


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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:
; NAME/KEY: intron
; LOCATION: 254..355
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..1715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start= 210
; OTHER INFORMATION: /product= "Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 210..380
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 381..1712
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "inositol phosphate
; OTHER INFORMATION: phosphatase"
; OTHER INFORMATION: /product= "Phytase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; US-08-151-574-31

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Query Match          99.8%; Score 1347; DB 1; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  CTGCGAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 63
Db      369 CTGCGAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 428

Qy      64  TGGCTCTCCGAGATTTCGATCTTTGGGTCATACGACCGTCTCTCTCTCTGGCAAC 123
Db      429 TGGCTCTCCGAGATTTCGATCTTTGGGTCATACGACCGTCTCTCTCTCTGGCAAC 488

Qy      124 GAATCGGTTCATCTCCCTCGAGGTGCCCGCGGATGCGAGTCACTTTCGTCAGGGTCCCTC 183
Db      489 GAATCGGTTCATCTCCCTCGAGGTGCCCGCGGATGCGAGTCACTTTCGTCAGGGTCCCTC 548

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Qy      184 TCCCGTCATGAGCGCGGTATCCGACCGGATCTCAAGGGCAAGAAATACTCCGCTCTCATTT 243
Db      549 TCCCGTCATGAGCGCGGTATCCGACCGGATCTCAAGGGCAAGAAATACTCCGCTCTCATTT 608

Qy      244 GAGGAGATCCAGCAGAACGGGACCACTTTGACGGGAAATATGCTTCTCTCAAGACATAC 303
Db      609 GAGGAGATCCAGCAGAACGGGACCACTTTGACGGGAAATATGCTTCTCTCAAGACATAC 668

Qy      304 AACTACAGCTTTGGGTGCAGATGACTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 363
Db      669 AACTACAGCTTTGGGTGCAGATGACTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 728

Qy      364 GGCATCAAGTTCTACCAAGCGGTAGCAATCGCTCAAGGACATCGTTCATTCATCCGA 423
Db      729 GGCATCAAGTTCTACCAAGCGGTAGCAATCGCTCAAGGACATCGTTCATTCATCCGA 788

Qy      424 TCCTCTGGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGGTTCACAGAGC 483
Db      789 TCCTCTGGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGGGTTCACAGAGC 848

Qy      484 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCAATGTCGCCCAAGATCGAGTGGTC 543
Db      849 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGGCAATGTCGCCCAAGATCGAGTGGTC 908

Qy      544 ATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCACTGTCTTGGAA 603
Db      909 ATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCACTGTCTTGGAA 968

Qy      604 GACAGCGAATTGGCGGATACCGTCCGAGCCAAATTTACCCGCCAGGTGTCGCCCTCATTT 663
Db      969 GACAGCGAATTGGCGGATACCGTCCGAGCCAAATTTACCCGCCAGGTGTCGCCCTCATTT 1028

Qy      664 GGTCAACGCTTGGAGACGACCTGTCGGTGTGACTCTCACAGACACAGAGATGACCTAC 723
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Qy      724 CTCATGGACATGTGCTCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGCC 783
Db      1089 CTCATGGACATGTGCTCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGCC 1148

Qy      784 CCCTTCTGTGACTGTTTACCCGATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 843
Db      1149 CCCTTCTGTGACTGTTTACCCGATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 1208

Qy      844 AAAAAAGTATTACGGCCATGTGTCAGGTAAACCGCTCGGCCGCGACCCAGGGGTGGCTAC 903
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Db 1689 GGTGATTGGCGGAGTGTTTTGCTTAG 1715

RESULT 7
US-08-419-448-31
; Sequence 31, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20008-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
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; LOCATION: 254..355
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; OTHER INFORMATION: /product= "Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
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; OTHER INFORMATION: phosphatase"
; OTHER INFORMATION: /product= "Phytase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; US-08-419-448-31

Query Match 99.8%; Score 1347; DB 2; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 63
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Qy 604 GACAGCGAATTTGGCCGATACCGTCAAGCCCAATTCACCGCCAGTTGTCCTCCATT 663
Db 969 GACAGCGAATTTGGCCGATACCGTCAAGCCCAATTCACCGCCAGTTGTCCTCCATT 1028
Qy 664 CGTCAAGCTCTGGAGAGGAGCTCTCGGGTGTGACTCTCAAGNACAGAGTGACCTAC 723
Db 1029 CGTCAAGCTCTGGAGAGGAGCTCTCGGGTGTGACTCTCAAGNACAGAGTGACCTAC 1088
Qy 724 CTCATGGACATGTGCTCTCTTCGACACCATCTCCACAGCACCGTTCGACCAAGTGTCC 783
Db 1089 CTCATGGACATGTGCTCTCTTCGACACCATCTCCACAGCACCGTTCGACCAAGTGTCC 1148
Qy 784 CCCTTCTGTGACCTGTTCAACCCATGAGAAATGATCACTACGACTACCTCCAGTCTTG 843
Db 1149 CCCTTCTGTGACCTGTTCAACCCATGAGAAATGATCACTACGACTACCTCCAGTCTTG 1208
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1209 AAAAGTATTACGGCCATGTCAGGTAAACCCGCTCGGCCGACCCAGCGCGTCGCTAC 1268
904 GCTAACGAGTATCGCCCGCTGACCCACTCGCCCTGTCACGATGACACCGAGTTCACAC 963
1269 GCTAACGAGTATCGCCCGCTGACCCACTCGCCCTGTCACGATGACACCGAGTTCACAC 1328
964 CACACTTTGAGCTCGAGCCCGGTACTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1023
1329 CACACTTTGAGCTCGAGCCCGGTACTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1388
1024 TCGATGACAAACGGCATCTCTCATCTCTTTTCTTTAGTCTGTACAAACGGCCTAAG 1083
1389 TCGCATGACAAACGGCATCTCTCATCTCTTTTCTTTAGTCTGTACAAACGGCCTAAG 1448
1084 CCCTATCTACACGACCGGAGATATCACCCAGACAGATGATCTCTCTCTCTGCTTGG 1143
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RESULT 8

US-09-233-510-31
Sequence 31, Application US/09233510
Patent No. 6350602
GENERAL INFORMATION:
APPLICANT: Robert P.M. Van Gorkom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seltin
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,510
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NRRL 3135
IMMEDIATE SOURCE:
LIBRARY: lambda AP
CLONE: pAF2-3, pAF2-6, pAF2-7
FEATURE:
NAME/KEY: exon
LOCATION: 210..253
FEATURE:
NAME/KEY: intron
LOCATION: 254..355
FEATURE:
NAME/KEY: exon
LOCATION: 356..1715
FEATURE:
NAME/KEY: CDS
LOCATION: join(210..253, 356..1715)
OTHER INFORMATION: /codon_start= 210
OTHER INFORMATION: /product= "Phytase"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 210..380
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 381..1712
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "inositol phosphate"
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OTHER INFORMATION: /evidence= EXPERIMENTAL
US-09-233-510-31

Query Match 99.8%; Score 1347; DB 3; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1269 GCTAACGAGCTCAGCGCGCTCAGCCACTCGCTGTCCAGATGACACAGTCCAAAC 1328
QY 964 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
DB 1329 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1388
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DB 1389 TCGCATGACACGCGATCATCTCAATCTCTTTGCTTTAGTCTGTGTACACGCGACTAG 1448
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DB 1569 CCGGTTGCTCGTGTCTTGGTTTAATGATCGGTTGCTCCCGTGTGATGGGTCTCCGTTGAT 1628
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DB 1629 GCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGGTGTAGCTTTGTAGATCTGGG 1688
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RESULT 9

US-07-923-724-7
; Sequence 7, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Maria T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Maria K.
; APPLICANT: Egerstr m, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923.724
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0240004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(404..447, 550..1906)
; US-07-923-724-7

Query Match 94.4%; Score 1275; DB 1; Length 2363;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Qy	304	AACTACAGCTTGGGTGCAGATGACTGACTCCCTTCGGAGAAACAGGAGCTAGTCAACTCC	363
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Qy	544	ATTTCGAGCGCCAGTCAATCCNCAACACATCTCGACCCAGCGCACTGCATGCTCTCGAA	603
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Qy	664	CGTCAAGTCTGGAGAACGACTGTCCGGTGTGACTCTCAACAGACAGAAAGTGACCTAC	723
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Db	1763	CCGCTGGTTCGGTTCGTTGTTAATGATCGCGTTGTCCCGCTGCATGGGTTCTCAATTGAT	1822

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Db	1823	GCNTTGGGAGAGTGTACCGGGATACCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG	1882
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RESULT 10
US-08-609-426A-7
; Sequence 7, Application US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(404..447, 550..1906)
US-08-609-426A-7

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; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(404..447, 550..1906)
; US-08-374-652C-1

Query Match          94.4%; Score 1275; DB 2; Length 2379;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1302; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTGGCATACGTCGATCGAGGGGTATCAA 63
Db 579 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTGGCATACGTCGATCGAGGGGTATCAA 638
QY 64 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGTTCTCTCTCTGGCAAC 123
Db 639 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGCGCGTTCTCTCTGGCAAC 698
QY 124 GAATCGGTCACTCCCGTGAAGTCCCGCCGGATGCAAGTCACTTTTCGCTCAAGTCCCTC 183
Db 699 GAATCGGCACTCTCCCGTGAAGTCCCGCCGGTTCAGAGTCACTTTTCGCTCAAGTCCCTC 758
QY 184 TCCCGTCAATGAGCGCGGTATCCGACGACTCCCAAGGCGAGAAATCTCGCTCAATT 243
Db 759 TCCCGTCAATGAGCGCGGTATCCGACGAGTCCCAAGGCGAGAAATCTCGCTCAATT 818
QY 244 GAGGAGATCCAGCAGAGACGCGACCACTTTGACCGGAAATATGCTTCCTGAAGACATAC 303
Db 819 GAGGAGATCCAGCAGAGACGCGTGAACACCTTTGATGAGAAATATGCTTCCTGAAGACATAC 878
QY 304 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGGAGAAAGAGAGCTAGTCAATCC 363
Db 879 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGGAGAGAGAGAGCTAGTCAATCC 938
QY 364 GGCATCAAGTCTTACCAGCGGTAGCAATCGCTCAAGGAACATCGTTTCCATTCAATCCGA 423
Db 939 GGCATCAAGTCTTACCAGCGGTAGCAATCGCTCAAGGAACATCAATCGTTTCAATCCGA 998
QY 424 TCCTCTGGCTCCAGCCCGGTGATCGCTCCCGGCAAGAAATTCATTCGAGGGCTTCAGAGC 483
Db 999 TCCTCTGGCTCCAGCCCGGTGATCGCTCCCGGCAAGAAATTCATTCGAGGGCTTCAGAGC 1058
QY 484 ACCAAGCTGAGGATCCTCGTCCCGACCGCCCAATCGTCGCCCAAGATCGAGTGGTC 543
Db 1059 ACCAAGCTGAGGATCCTCGTCCCGACCGCCCAATCGTCGCCCAAGATCGAGTGGTC 1118
QY 544 ATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGCACCTGCACTGTCTTCGAA 603
Db 1119 ATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGCACCTGCACTGTCTTCGAA 1178
QY 604 GACAGCAATTTGGCGGATACCGTGAAGCCAAATTCACCGCCAGTTCGTCCTCCATT 663
Db 1179 GACAGCAATTTGGCGGATACCGTGAAGCCAAATTCACCGCCAGTTCGTCCTCCATT 1238
QY 664 CGTCAACGCTCGGAGAACGACTCTGCGGTGTGACTCTCAAGACACAGAAAGTGAACCTAC 723
Db 1239 CGTCAACGCTCGGAGAACGACTCTGCGGTGTGACTCTCAAGACACAGAAAGTGAACCTAC 1298
QY 724 CTCATGACATGTGCTCTTCGACACCATCTCCACGACCGGTGACACCAAGCTGTCC 783
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QY 784 CCGTTCTGTGACCTGTTCAACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 843
Db 1359 CCGTTCTGTGACCTGTTCAACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 1418
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QY 844 AAAAGTATTACGGCCATGTCAGGTAAACCGCTCGGCCGACCCAGCGGCGTCGGCTAC 903
Db 1419 AAAAATACTACGGCCATGTCGAGGTAAACCGCTCGGCCGACCCAGCGGCGTCGGCTAC 1478
QY 904 GTTAACGAGCTCATCGCCGTCGTGACCCACTCGCCTGTCCAGATGACACCAAGTTCACAA 963
Db 1479 GTTAACGAGCTCATCGCCGTCGTCAACCACTCGCCTGTCCAGATGACACCAAGTTCACAA 1538
QY 964 CACACTTTGGACTCGAGCCCGGCTACCTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1539 CACACTTTGGACTCGAAGCCAGCTACCTTCCCGCTCAACTCTACTCTCTACGGGACTTT 1598
QY 1024 TCGCATGACAAAGCGCATCATCTCCATTTCTTTGCTTTAGTGCTCTTACAAAGCGCTAAG 1083
Db 1599 TCCACGATAACGGCATCATCTCTATCTCTTTGCTTTGGGTCTGTACAAAGCGCTAAG 1658
QY 1084 CGCTATCTACACGACCGGTGAGAAATATCAACCCAGACAGATGGAATTCCTCTCTGTTGG 1143
Db 1659 CGCTGTCTACACGACCGGTGAGAAATATCAACCCAGACAGATGGAATTCCTCTCTGTTGG 1718
QY 1144 ACGTTTCCGTTTGGCTTTCGGGTTTGTACGTCGAGATGATGACGTGTCAAGCGGAGCAGGAG 1203
Db 1719 ACGTTTCCGTTTGGCTTTCGGGTTTGTACGTCGAGATGATGACGTGTCAAGCGGAGCAGGAG 1778
QY 1204 CGCTGGTCCGCTGCTTGGTTAATGATCGCTTGTCCCGCTGCATGGGTGTCGGTGTGAT 1263
Db 1779 CGCTGGTCCGCTGCTTGGTTAATGATCGCTTGTCCCGCTGCATGGGTGTCGGTGTGAT 1838
QY 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGGTTCAGCTTTGCTAGATCTGGG 1323
Db 1839 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGGTTCAGCTTTGCTAGATCTGGG 1898
QY 1324 GGTGATTGGCGGAGTGTGTTTTCCTTAG 1350
Db 1899 GGTGATTGGCGGAGTGTGTTTTCCTTAG 1925

RESULT 12
US-09-155-855-5
; Sequence 5, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
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FEATURE: ;
NAME/KEY: CDS ;
LOCATION: (157)..(1512) ;
US-09-155-855-5 ;

Query Match
Best Local Similarity 87.6%; Score 1182.2; DB 3; Length 1515;
; Pred. No. 2.5e-301;
Matches 1244; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGTATCAA 63
DB 169 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGTATCAA 228

QY 64 TGTCTTCGAGACTTCGATCTTGGGGTCAATACGACCCGTTCTTCTCTCGGCAAC 123
DB 229 TGTCTTCGAGACTTCGATCTTGGGGTCAATACGACCCGTTCTTCTCTCGGCAAC 288

QY 124 GAATCGGTATCTCCCTGAGGTGCGCCGCGATGCGAGTCACTTTGCTCAGGTCTTC 183
DB 289 AAATCGGCATCTCCCTGATGTTCCTGCGGATGCCATGTCACTTTGCGCCAGGTCTC 348

QY 184 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAGGCGAAGAAATCTCCGCTCTCAT 243
DB 349 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAGGCGAAGAAATCTCCGCTCTCAT 408

QY 244 GAGGAGATCCAGCAACCGGACCACTTTGACGGAATAATGCTTCTGGAAGACATAC 303
DB 409 GAGGAGATCCAGCAACCGGACCACTTTGAGGGGAATAATGCTTCTGGAAGACATAC 468

QY 304 AACTACAGTTCGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTAGTCAATCC 363
DB 469 AACTACAGTTCGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGTAGTCAATCC 528

QY 364 GGCATCAAGTTCACACCGGTAGCAATCGCTCAAGGAACATCGTTTCCATTCATCCGA 423
DB 529 GGCATCAAGTTCACACCGGTAGCAATCGCTCAAGGAACATCGTTTCCATTCATCCGA 588

QY 424 TCCTCGGCTCAGCGCGGTATCGCTCCGCGAAGAAATTCATCGAGGGTTCAGAGC 483
DB 589 TCCTCGGCTCAGCGCGGTATCGCTCCGCGAAGAAATTCATCGAGGGTTCAGAGC 648

QY 484 ACCAAGCTGAGAGTCTCTGTCGCGCCAGCCGCGCAATCGTCCGCAAGATCGAGTGGTC 543
DB 649 ACTAAGCTGAGAGTCTCTGTCGCGCCAGCCGCGCAATCGTCCGCAAGATCGAGTGGTC 708

QY 544 ATTTCCGAGGCGAGTCAATCAACAACTCTCGACCCAGGCACTGCACTGTCTTCGAA 603
DB 709 ATTTCCGAGGCGAGTCAATCAACAACTCTCGACCCAGGCACTGCACTGTCTTCGAA 768

QY 604 GACAGCGAATGGCGATACCGTTCGAGGCAATTTCAAGCCAGTTCGTCCTCCAT 663
DB 769 GACAGCGAATGGCGATACCGTTCGAGGCAATTTCAAGCCAGTTCGTCCTCCAT 828

QY 664 CGTCAACCTCTGGAGACGACTCTCGGTGTGACTCTCAAGACAGAGTCAAGTCACTAC 723
DB 829 CGTCAACCTCTGGAGACGACTCTCGGTGTGACTCTCAAGACAGAGTCAAGTCACTAC 888

QY 724 CTCATGAGATGTCTCTTCGACACCACTTCACACGACCGTTCGACACCAAGTCTGC 783
DB 889 CTCATGAGATGTCTCTTCGACACCACTTCACACGACCGTTCGACACCAAGTCTGC 948

QY 784 CCGTCTCTGTGACTCTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 843
DB 949 CCGTCTCTGTGACTCTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 1008

QY 844 AAAAGTATTACGCCATGTTGAGGTAACCGCTCGGCGCCAGCCAGGGGTGGGTAC 903
DB 1009 AACAAATCTACGGGCATGGCGCAGGTAAACCGCTCGGCGCCAGCCAGGGGTGGGTAC 1068

QY 904 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGGCTGTCCACGATGACACGAGTTCAC 963
DB 1069 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGGCTGTCCACGATGACACGAGTTCAC 1128

QY 964 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTCTACTCTCTACCGGACTTT 1023
DB 1129 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTCTACTCTCTATCGGACTTT 1188

QY 1024 TGCATGACAAACGGCATCATCTCTCTTTGCTTTAGTCTGTATCAACAGGCACTAAG 1083
DB 1189 TGCATGACAAACGGCATCATCTCTCTTTGCTTTAGTCTGTATCAACAGGCACTAAG 1248

QY 1084 CGGCTATCTACACACCGTGGAGAAATACCCAGACAGATGGATCTCTGCTCTCTGG 1143
DB 1249 CGGCTATCTACACACCGTGGAGAAATACCCAGACAGATGGATCTCTGCTCTCTGG 1308

QY 1144 ACGGTTCCGTTTTCGCTTCGCTTTGACGTCGAGATGATGACGTCGAGGAGGAG 1203
DB 1309 ACGGTTCCGTTTTCGCTTCGCTTTGACGTCGAGATGATGACGTCGAGGAGGAG 1368

QY 1204 CGGCTGTCGCTGCTCTGTTTAATGATCGGCTGTCGCTGTCATGGGTTCCTGGTTGAT 1263
DB 1369 CTTTGGTCCGTTGCTGTTTAATGATCGGCTGTCGCTGTCATGGGTTCCTGGTTGAT 1428

QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTGTAGGGGTTGAGCTTTGCTAGATCTGG 1323
DB 1429 GCTTTGGGAGATGTACCCGGGATAGCTTTGTAGGGGTTGAGCTTTGCTAGATCTGG 1488

QY 1324 GGTGATTGGCGGAGTGTTCCTTAG 1350
DB 1489 GGTGATTGGCGGAGTGTTCCTTAG 1515

RESULT 13
US-09-543-744-5
; Sequence 5, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANBE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-543-744-5

Query Match 87.6%; Score 1182.2; DB 3; Length 1515;
Best Local Similarity 92.4%; Pred. No. 2.5e-301;
Matches 1244; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGTATCAA 63
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QY 64 TGCTTCTCCGAGACTTCGGATCTTTGGGTCATATGACACCGTTCCTCTCTGCGCAAC 123
Db 229 TGCTTCTCGGAGACTTCGGATCTTTGGGTCATATGACACCGTTCCTCTCTGCGCAAC 288
QY 124 GAATCGGTCTATCTCCCTGAGGTGCGCGCGGATGACAGTCACTTTCGTTCAGGTCCTC 183
Db 289 AATCGGCATCTCCCTGATGTTCTGCGGATGCCATGCTACTTTCGCCAGGTTCTC 348
QY 184 TCCGTCATGAGCGCGGTATCCGACCGATCCAAAGGCAAGAAATACCTCCGTCCTCAT 243
Db 349 TCCGCCATGAGCAGCGTATCCGACCGATCCAAAGGCAAGAAATACCTCCGTCCTCATC 408
QY 244 GAGGAGATCCAGCAGCAGCGGACACCTTTGACGGAATATGCTTCTGGAAGACATAC 303
Db 409 GAGGAGATCCAGCAGCAGCGGACACCTTTGACGGAATATGCTTCTGGAAGACATAC 468
QY 304 AACTACAGTCTGGTGCAGATGACCTGACTCCCTTCGGAGAAACAGGAGTGTCAACTCC 363
Db 469 AACTACAGTCTGGTGCAGATGACCTGACTCCCTTCGGAGAGAGAGTGTCAACTCC 528
QY 364 GGCATCAAGTCTACACGCGGTAGCATCGCTCACAGGAACATCGTTCCTCATTCATCCGA 423
Db 529 GCGTCAAGTCTACACGCGGTAGCATCGCTCACAGGAACATCGTTCCTCATTCATCCGA 588
QY 424 TCCTCTGGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGCTTCAGAGC 483
Db 589 TCCTCAGCTCCAGCCGCGTATCGCTCCGCGCAAGAAATTCATCGAGGCTTCAGAGC 648
QY 484 ACCAAGCTGAAGATCTCTGTGCGGCGCGGCAATCGTTCGCGCAAGATCGAGTGGTC 543
Db 649 ACTAAGCTGAAGATCTCTGTGCGGCGCGGCAATCGTTCGCGCAAGATCGAGTGGTC 708
QY 544 ATTTCCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGCACTCTCACTGTCTTCGAA 603
Db 709 ATTTCCGAGGCGAGCACTCAACAACTCTCGATCGGCGCACTCTCACTGTCTTCGAA 768
QY 604 GACAGCAATTCGCGGATACGTCGAAGCCAAATTCACCGCCAGCTTCGTCCTCCCTCAT 663
Db 769 GATAGCAATTCGCGGATACGTCGAAGCCAAATTCACCGCCAGCTTCGTCCTCCCTCAT 828
QY 664 CGTCAAGCTTCGAGAGAGGCTTCGCGGTGATCTCTCAGACAGAGTGTACCTAC 723
Db 829 CGTCAAGCTTCGAGAGAGGCTTCGCGGTGATCTCTCAGGACAGAGTGTACCTAC 888
QY 724 CTCTAGGACATGTCTCTTCGACACCATCTCCACGACCGCTCGACACCAAGCTGTCC 783
Db 889 CTCTAGGACATGTCTCTTCGACACCATCTCCACGACCGCTCGACACCAAGCTGTCC 948
QY 784 CCCTTCTGTGACCTGTTCACCATGACGAATGGATCACTACGACTACCTCCAGTCTTG 843
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QY 844 AAAAAGTATTACGCCATGTTGAGGTAAACCGCTCGGCGGACCCAGGCGTCGGCTAC 903
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QY 904 GCTAACAGCTCATCGCCGCTGACCACTGCGCTGTCCAGATGACACAGTTCACAC 963
Db 1069 GCTAACAGCTCATCGCCGCTGACCACTGCGCTGTCCAGATGACACAGTTCACAC 1128
QY 964 CACATTTGGACTCGAGCCCGGCTACCTTTCGCTCACTCACTCTCTACCGGACTTT 1023
Db 1129 CACATTTGGACTCGAGCCCGGCTACCTTTCGCTCACTCACTCTCTACCGGACTTT 1188
QY 1024 TCGCATGACAAAGGCGATCATCTCATCTCTTTGCTTTAGTCTGTATCAAGCGCACTAAG 1083
Db 1189 TCGCATGACAAAGGCGATCATCTCATCTCTTTGCTTTGGTGTGTATCAAGCGCACTAAG 1248
QY 1084 CCGCTATCTACACGACCGTGAGATATACCCAGCAGATGATCTCTGCTGCTTGG 1143
Db 1249 CCGCTGTCTTCCAGACCGGAGATATACCCAGCAGATGATCTCTGCTGCTTGG 1308

QY 1144 ACGGTTCCGTTTGGTTCGCTTGTACGTCAGATGATGACGTCAGTCGAGCAGGAG 1203
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Db 1369 CCGTTGGTCCGCTTGTAAATGATCGCTTGTCCCGTCGATGGGTGTCGCTTGTAT 1428
QY 1264 GCTTTGGGAGATGATACCCGGGATGCTTGTGAGGGGTTGAGCTTTGTAGATCTCGG 1323
Db 1429 GCTTTGGGAGATGATACCCGGGATGCTTGTGAGGGGTTGAGCTTTGTAGATCTCGG 1488
QY 1324 GGTGATTGGCGGAGTGTGCTTTAG 1350
Db 1489 GGTGATTGGCGGAGTGTGCTTTAG 1515

RESULT 14
US-09-929-060-5
; Sequence 5, Application US/09929060
; Patent No. 6548282
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEWASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929, 060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543, 744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155, 855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-929-060-5

Query Match 87.6%; Score 1182.2; DB 4; Length 1515;
Best Local Similarity 92.4%; Pred. No. 2.5e-301; Mismatches 103; Indels 0; Gaps 0;
Matches 1244; Conservative 0;

QY 4 CTGGCAGTCCCGCTTCGAGAAATCAATCCAGTTGCGATACGTCGATCAGGGGTATCAA 63
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QY 64 TGCTTCTCGAGACTTCGCTTGGGTCATGTCAGCACCCTTCTCTCTGCGCAAC 123
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Db 289 AATCGGCTATCTCCCTGATGTTCTCGGATGCCATGTCATTTGCCAGGTTCTC 348
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Db 349 TCCGTCATGAGCAGCGTATCGACCGCTCAAGGGCAAGAAATCTCCGCTCTCATC 408
QY 244 GAGGATCCAGCAGACCGCCTTTGAGGAAATATGCTTCTGAGACATAC 303
Db 409 GAGGATCCAGCAGACCGCCTTTGAGGAAATATGCTTCTGAGACATAC 468

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QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGGAGTACTAGTCACTCC 363
Db 469 AACTACAGCTGGGCGGGATGATCTGACTCCCTTCGGAGAGAGAGCTGCTCACTCC 528
QY 364 GGCATCAAGTTCTACAGCGGTGAGATCGCTTCAGAGAAATCGTTTCCATTCACCGA 423
Db 529 GCGCTCAAGTTCTACAGCGGTGAGATCGCTTCAGAGAAATCGTTTCCATTCACCGA 588
QY 424 TCCTCTGCTCCAGCGGTGATCGCTTCGGCAGAAATTCATCGAGGGTTCAGAGC 483
Db 589 TCCTCAGGCTCAGCGGTGATCGCTTCGGCAGAAATTCATCGAGGGTTCAGAGC 648
QY 484 ACCAAGCTGAAGATTCCTGCTGCCAGCGCGGCAATCGTCCGCCAAGATCGAGTGGTC 543
Db 649 ACTAAGCTGAAGATTCCTGCTGCCAGCGCGGCAATCGTCCGCCAAGATCGAGTGGTC 708
QY 544 ATTTCCGAGGCGAGCTGATCCAAACAACACTCTCGACCGAGCAGTGTCTTCGAA 603
Db 709 ATTTCCGAGGCGAGCAGATCCAAACAACACTCTCGATCCGGCAGCTGCACCGTTTCGAA 768
QY 604 GACAGCAATGGCCGATACCGTCCGAAGCAATTTCAACGCCAGTTCGTCCCTCCATT 663
Db 769 GATACGAAATGGCGATGATCGAGCCATTTTCAACGCCAGTTCGTCCCTCCATT 828
QY 664 CGTCAACGTCTGGAGAACGACTGTCGGGTGTGACTCTCAAGACAGAGTACCTAC 723
Db 829 CGTCAACGTCTGGAGAACGACTGTCGGGTGTGACTCTCAAGACAGAGTACCTAC 888
QY 724 CTCATGACATGTGCTCTCGACACCACTCTCCACCGACCGTCCGACACCAAGCTGCC 783
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QY 784 CCCTTCTGTGACCTGTTCAACCCATGAGAAATGGAATCAACTACGACTACCTCCAGTCTTG 843
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QY 844 AAAAGTATTACGCCATGTTGAGGTAAACCGCTCCGCCCGACCGAGGGGTGGGTAC 903
Db 1009 AAAAGTATTACGCCATGTTGAGGTAAACCGCTCCGCCCGACCGAGGGGTGGGTAC 1068
QY 904 GCTAACGAGCTCATCGCCGCTGTACCCACTCTGTCACCGATGACACAGTTCACAC 963
Db 1069 GCTAACGAGCTCATCGCCGCTGTACCCACTCTGTCACCGATGACACAGTTCACAC 1128
QY 964 CACACTTGGAGTACGAGCGCGGTACCTTCCGCTCAACTCTACTCTCTACGCGACTTT 1023
Db 1129 CACACTTGGAGTACGAGCGCGGTACCTTCCGCTCAACTCTACTCTCTACGCGACTTT 1188
QY 1024 TCGCATGACAAAGGATCATCTCCATCTCTTTGCTTTAGTCTGTGTACACCGCACTAAG 1083
Db 1189 TCGCATGATACAGGATCATCTCTCTCTTTGCTTTAGTCTGTGTACACCGCACTAAG 1248
QY 1084 CCGCTATCTACAGCGGTGGAGATATACCCAGACAGATGATTTCTGCTGTGTGG 1143
Db 1249 CCGCTGTCTTCCAGCGCGGAGATATACCCAGACCGATGGTCTCATCTGCTGTG 1308
QY 1144 ACGGTTCGGTGTGCTCGCTTTCTGCTGAGATGATGAGTGTACAGGCGGAGCAGGAG 1203
Db 1309 ACGGTTCGGTGTGCTCGCTTTCTGAGGGGTGAGCTTTGCTAGATCTGG 1368
QY 1204 CCGTGTGCTGTCTTGGTTAATGATCGGCTGTGCTCCGCTGATGGGTGCTCGGTTGAT 1263
Db 1369 CCGTGTGCTGTCTTGGTTAATGATCGGCTGTGCTCCGCTGATGGGTGCTCGGTTGAT 1428
QY 1264 GCTTTGGGAGATGATACCGGATAGCTTTGAGGGGTGAGCTTTGCTAGATCTGG 1323
Db 1429 GCTTTGGGAGATGATACCGGATAGCTTTGAGGGGTGAGCTTTGCTAGATCTGG 1488
QY 1324 GGTGATTGGGCGAGTGTGTTTGGCTTAG 1350
Db 1489 GGTGATTGGGCGAGTGTGTTTGGCTTAG 1515
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RESULT 15
US-09-155-855-4
; Sequence 4, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; EARLIER FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-155-855-4
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Query Match 86.5%; Score 1167.2; DB 3; Length 1332;
Best Local Similarity 92.3%; Pred. No. 2.1e-297;
Matches 1229; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
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QY 79 TCGCATTTTGGGGTCAATAGCACCGTTCTTCTCTTGGCAAGAAATCGGTATCTCC 138
Db 61 TCGCATTTTGGGGCAATAACGGCGTTCTTTCTTGGCAAAATAATCGGCATCTCC 120
QY 139 CTGAGGTGCGCGCGGATGACAGTCTTTCGTCTAGGTCTCTCCCGTCATGGAGCG 198
Db 121 CTTGATGTTCTCGCGATGCGATGCTCACTTTCGCGAGGTTCTCTCCCGATGGAGCA 180
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16	1343.8	99.5	2665	17	US-10-662-914-31	Sequence 31, Appl
17	1343.8	99.5	2665	17	US-10-662-914-35	Sequence 35, Appl
18	1343.8	99.5	2665	17	US-10-662-914-39	Sequence 39, Appl
19	1343.8	99.5	2665	17	US-10-662-914-41	Sequence 41, Appl
20	1343.8	99.5	2665	17	US-10-662-914-43	Sequence 43, Appl
21	1342.2	99.4	2665	17	US-10-662-914-37	Sequence 37, Appl
22	1342.2	99.4	2665	17	US-10-662-914-45	Sequence 45, Appl
23	1342.2	99.4	2665	17	US-10-662-914-49	Sequence 49, Appl
24	1342.2	99.4	2665	17	US-10-662-914-51	Sequence 51, Appl
25	1342.2	99.4	2665	17	US-10-662-914-47	Sequence 47, Appl
26	1340.6	99.3	2665	17	US-10-662-914-53	Sequence 53, Appl
27	1340.6	99.3	2665	17	US-10-662-914-55	Sequence 55, Appl
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30	1167.2	86.5	1332	9	US-09-929-060-4	Sequence 4, Appl
31	659.8	48.9	1426	15	US-10-442-538-168	Sequence 168, App
32	636.2	47.1	1401	17	US-10-662-914-13	Sequence 13, Appl
33	636.2	47.1	1567	14	US-10-082-848-13	Sequence 13, Appl
34	636.2	47.1	1567	17	US-10-776-104-13	Sequence 13, Appl
35	621.4	46.0	1404	15	US-10-442-538-162	Sequence 162, App
36	613.4	45.4	1426	15	US-10-421-112-3	Sequence 3, Appl
37	613.4	45.4	1426	15	US-10-442-538-117	Sequence 117, App
38	608.6	45.1	1426	15	US-10-442-538-140	Sequence 140, App
39	602	44.6	1404	15	US-10-442-538-164	Sequence 164, App
40	600	44.4	1404	15	US-10-442-538-166	Sequence 166, App
41	600	44.4	1425	14	US-10-213-990-23	Sequence 23, Appl
42	600	44.4	1425	14	US-10-213-990-22	Sequence 22, Appl
43	598.4	44.3	1455	14	US-10-662-914-3	Sequence 3, Appl
44	598.4	44.3	1571	14	US-10-062-848-10	Sequence 10, Appl
45	598.4	44.3	1571	17	US-10-776-104-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-079-709-33
; Sequence 33, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seiten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578

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Perfect score: 1350
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 7280484

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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15:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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19:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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21:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1347	99.8	2665	17	US-10-662-914-1
3	1347	99.8	6756	15	US-10-079-709-31
4	1345.4	99.7	2665	17	US-10-662-914-5
5	1345.4	99.7	2665	17	US-10-662-914-7
6	1345.4	99.7	2665	17	US-10-662-914-11
7	1345.4	99.7	2665	17	US-10-662-914-17
8	1345.4	99.7	2665	17	US-10-662-914-19
9	1345.4	99.7	2665	17	US-10-662-914-21
10	1345.4	99.7	2665	17	US-10-662-914-23
11	1345.4	99.7	2665	17	US-10-662-914-25
12	1345.4	99.7	2665	17	US-10-662-914-27

; FILING DATE: 24-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Muraehige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20026.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-327-7250
 ; TELEFAX: 415-327-2951
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORGANISM: Aspergillus ficuum (Aspergillus niger)
 ; STRAIN: NRRL 3135
 ; US-10-079-709-33

Query Match 99.8%; Score 1347; DB 15; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	304	AATACAGCTTTGGGTGAGATGACCTGACCTCCCTTCGAGAACAGGAGTGTCAACTCC	363
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Qy	424	TCCTCTGGCTCCAGCGCGTATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC	483
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Qy	484	ACCAAGCTGAAGATTCCTGTCGCGAGCGCGCAATTCGTCGCGCAAGATCGACGTGTC	543
Db	538	ACCAAGCTGAAGATTCCTGTCGCGAGCGCGCAATTCGTCGCGCAAGATCGACGTGTC	597
Qy	544	ATTTCCGAGCGAGCTCATCAACACATCTCGACCCGACCTGCACTGCTTCGAA	603
Db	598	ATTTCCGAGCGAGCTCATCAACACATCTCGACCCGACCTGCACTGCTTCGAA	657
Qy	604	GACAGGAATGCGCGATACCGTCAAGCCAAATTCACCGCCACGTTTCGTCCTCCAT	663
Db	658	GACAGGAATGCGCGATACCGTCAAGCCAAATTCACCGCCACGTTTCGTCCTCCAT	717
Qy	664	CGTCAAGCTCTGAGACGACCTGTCGGGTGACTCTCACAGACACAGAGTGACCTAC	723
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Qy	724	CTCATGACATGTCTCTTTCGACACCATCTCCACGACACCGTTCGACACCAAGTGTCC	783
Db	778	CTCATGACATGTCTCTTTCGACACCATCTCCACGACACCGTTCGACACCAAGTGTCC	837
Qy	784	CCCTTCTGTGACCTGTTTACCCATGACGAATGATCACTAGACTACTCCAGTCTTG	843
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Qy	844	AAAAAGTATTAGCGCATGTCAGGTACCGCTCGGCCCGACACGAGCGCTCGGCTAC	903
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Qy	904	GCTAACGAGCTCATGCCCGTCTGACCCACTCGCTGTCACGATGACACAGTTCGAAC	963
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Qy	964	CACACTTTGAGTCTCGAGCCCGCTACCTTTCCGCTCACTCTCTCTACCGGACTTT	1023
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Qy	1084	CGGCTATCTACACACCGTGGAGATATACCCAGACAGATGGATTCTCTCTGCTTGG	1143
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Db	1198	ACGTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG	1257
Qy	1204	CGGCTGCTCGGCTGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG	1263
Db	1258	CGGCTGCTCGGCTGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG	1317
Qy	1264	GCTTTGGGAGATGATACCCGGATAGCTTTTGTAGGGGGTTCGCTTTCGCTTTCGCTTTCG	1323
Db	1318	GCTTTGGGAGATGATACCCGGATAGCTTTTGTAGGGGGTTCGCTTTCGCTTTCGCTTTCG	1377
Qy	1324	GCTGATTGGCGGAGTGTTCCTTAG 1350	
Db	1378	GCTGATTGGCGGAGTGTTCCTTAG 1404	

RESULT 2
 US-10-662-914-1
 ; Sequence 1, Application US/10662914
 ; Publication No. US20040126844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lei, Xingen
 ; APPLICANT: Mullane, Edward J.
 ; APPLICANT: Ullah, Abul H.J.
 ; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTAES
 ; FILE REFERENCE: 19603/4261
 ; CURRENT APPLICATION NUMBER: US/10/662,914
 ; PRIOR FILING DATE: 2003-09-15
 ; PRIOR APPLICATION NUMBER: 60/410,736
 ; PRIOR FILING DATE: 2002-09-13
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2685
 ; TYPE: DNA
 ; ORGANISM: Aspergillus niger
 ; US-10-662-914-1

Query Match 99.8%; Score 1347; DB 17; Length 2665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 124 GAATCGGTATCTCCCTGAGGTGCGCGCGGATGAGAGTCACTTTCGTCAGGTCCTC 183
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Qy 184 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGCAAGAAATACCTCCGCTCTCAT 243
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Qy 364 GGATCAAGTTTACAGCGGTAGGAATCGCTACAGGAACATCGTTCATTCATCCGA 423
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Db 1382 ATTTCCGAGCGACTCATCAACACACTCTGACCCAGCAGCTCAGCTGTCTCGAA 1441
Qy 604 GACAGCAATTTGGCGGATACCGTCCGAAGCCAAATTTACCGCCAGCTTCGTCCTCCATT 663
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Qy 664 CGTCAACGCTCGAGAACAGCTGTCGGGTGATCTCTCACAGACAGAGTGAACCTAC 723
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Db 1562 CTCATGGACATGTCTCTTCGACACCATCTCCACAGCAGCCGTCGACACCAAGCTCTCC 1621
Qy 784 CCCTTCTGTGACCTGTTCAACCATGAGAAATGGATCAACTAGACTACCTCCAGTCTTG 843
Db 1622 CCCTTCTGTGACCTGTTCAACCATGAGAAATGGATCAACTAGACTACCTCCAGTCTTG 1681
Qy 844 AAAAAGTATTACGCCATGTCGAGTAAACCGCTCGSCCGGACCCAGGGGTGCGGTAC 903
Db 1682 AAAAAGTATTACGCCATGTCGAGTAAACCGCTCGSCCGGACCCAGGGGTGCGGTAC 1741
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Db 1982 ACGGTTCCGTTTGTCTTCGCGTTTGTACGTCGAGATGATGAGTGTACAGCGGACAGAG 2041
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Db 2162 GGTGATTGGCGGAGTGTTCCTTGTAG 2188

RESULT 3

US-10-079-709-31
; Sequence 31, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Faridon
; APPLICANT: Anemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficum (Aspergillus niger)

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/ STRAIN: NRRL 3135
/ IMMEDIATE SOURCE:
/ LIBRARY: lambda AP
/ CLONE: pAF2-3, pAF2-6, pAF2-7
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/ NAME/KEY: exon
/ LOCATION: 210..253
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 254..355
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 356..1715
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: join(210..253, 356..1715)
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/ OTHER INFORMATION: /product= "Phytase"
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 210..380
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 381..1712
/ IDENTIFICATION METHOD: experimental
/ OTHER INFORMATION: /function= "inositol phosphate
/ OTHER INFORMATION: /product= "Phytase"
/ OTHER INFORMATION: /evidence= EXPERIMENTAL
US-10-079-709-31

Query Match 99.8%; Score 1347; DB 15; Length 6756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 63
DB 369 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAA 428
QY 64 TGGTTCTCCGAGATTTCGCAATCTTTGGGTCAATPACGACCGTTCTTCTCTCTGGCAAAAC 123
DB 429 TGGTTCTCCGAGATTTCGCAATCTTTGGGTCAATPACGACCGTTCTTCTCTCTGGCAAAAC 488
QY 124 GAATCGGTCAATCCCTGAGTCCCGCGGATGCGAGTCACTTTTCGCTCAGGTCTTC 193
DB 489 GAATCGGTCAATCCCTGAGTCCCGCGGATGCGAGTCACTTTTCGCTCAGGTCTTC 548
QY 184 TCCCGTTCATGAGCGCGGTATCCGACCGACTCCAAAGGCGCAAGAAATACCTCCGCTCTCAAT 243
DB 549 TCCCGTTCATGAGCGCGGTATCCGACCGACTCCAAAGGCGCAAGAAATACCTCCGCTCTCAAT 608
QY 244 GAGGAGATCCAGCAGACGCGACCACTTTTGAAGGAAATATGCTTCTCTGAAAGACATAC 303
DB 609 GAGGAGATCCAGCAGACGCGACCACTTTTGAAGGAAATATGCTTCTCTGAAAGACATAC 668
QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCAACTCC 363
DB 669 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCAACTCC 728
QY 364 GGCATCAAGTTTACACGCGGTACGATCGCTCACAGGAACATCGTTTCATTCATCCGA 423
DB 729 GGCATCAAGTTTACACGCGGTACGATCGCTCACAGGAACATCGTTTCATTCATCCGA 788
QY 424 TCCTCTGGCTCCAGCGCGGTATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 483
DB 789 TCCTCTGGCTCCAGCGCGGTATCGCTCCGCAAGAAATTCATCGAGGCTTCCAGAGC 848
QY 484 ACCAAGCTGAAGATCTCTGTCGCCAGCCCGCAATCGTCGCCCAAGATCGACGTGGTC 543
DB 849 ACCAAGCTGAAGATCTCTGTCGCCAGCCCGCAATCGTCGCCCAAGATCGACGTGGTC 908
QY 544 ATTTCCGAGCCAGCTCATCCACACACTCTCGACCCAGGACCTGCACTCTTCGAA 603
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DB 969 GACAGCAATTGGCCGATACCGTTCGAAGCAATTTTACCGCCACAGTTTCTGTCCTCCATT 1028
QY 664 CGTCAACGTTCTGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAAATGACCTAC 723
DB 1029 CGTCAACGTTCTGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAAATGACCTAC 1088
QY 724 CTCATGGACATGTCTTTCGACACCACTCTCCACAGCAGCCGTGCGACACCAAGTGTCC 783
DB 1089 CTCATGGACATGTCTTTCGACACCACTCTCCACAGCAGCCGTGCGACACCAAGTGTCC 1148
QY 784 CCCTTCTGTGACTGTTTACCCATGACGAAATGATCACTAGACTACCTCAGTCTCTTG 843
DB 1149 CCCTTCTGTGACTGTTTACCCATGACGAAATGATCACTAGACTACCTCAGTCTCTTG 1208
QY 844 AAAAGTATTACGGCCATGTTGTCAGGTAAACCGCTCGGCCCGGACCCAGGGGCTCGCTAC 903
DB 1209 AAAAGTATTACGGCCATGTTGTCAGGTAAACCGCTCGGCCCGGACCCAGGGGCTCGCTAC 1268
QY 904 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTCTGTCACGATGACACAGTTTCCAAC 963
DB 1269 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTCTGTCACGATGACACAGTTTCCAAC 1328
QY 964 CACACTTTGGACTCGAGCCCGGTACTCTTTCGGCTCAACTCTACTCTCTAGCGGACTTT 1023
DB 1329 CACACTTTGGACTCGAGCCCGGTACTCTTTCGGCTCAACTCTACTCTCTAGCGGACTTT 1388
QY 1024 TCGCATGACACGGCATCATCTCTCTTTTGTCTTTAGTCTGTATCAACGGGCACTAAG 1083
DB 1389 TCGCATGACACGGCATCATCTCTCTTTTGTCTTTAGTCTGTATCAACGGGCACTAAG 1448
QY 1084 CGCTATCTACACAGCCGTGGAGATATACCCAGAGATGATGATGATGATGATGATGATGAT 1143
DB 1449 CGCTATCTACACAGCCGTGGAGATATACCCAGAGATGATGATGATGATGATGATGATGAT 1508
QY 1144 ACGGTTCCGTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1203
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QY 1204 CGCTGTTCCGTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1263
DB 1569 CGCTGTTCCGTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1628
QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTCGAGGGGTTGAGCTTTCGATATCTGGG 1323
DB 1629 GCTTTGGGAGATGTACCCGGGATAGCTTTCGAGGGGTTGAGCTTTCGATATCTGGG 1688
QY 1324 GGTGATTCGGGCGAGTGTTCGCTTAG 1350
DB 1689 GGTGATTCGGGCGAGTGTTCGCTTAG 1715

RESULT 4
US-10-662-914-5
; Sequence 5, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H. J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2665
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; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-5

Query Match      99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 63
Db  842 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 901

Qy  64 TGCTTCTCCGAGACTTCGGCATCTTTGGGGTCAATPACACACCGTTCTTCTCTCTGGCAAAAC 123
Db  902 TGCTTCTCCGAGACTTCGGCATCTTTGGGGTCCATPACACACCGTTCTTCTCTCTGGCAAAAC 961

Qy  124 GAATCGGTCAATCTCCCTGAGGTGCCCGCGGATGCAGATCACTTCGTCAGGTCCTC 183
Db  962 GAATCGGTCAATCTCCCTGAGGTGCCCGCGGATGCAGATCACTTCGTCAGGTCCTC 1021

Qy  184 TCCCGTCAATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATACTCCGCTCTCAAT 243
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Qy  244 GAGGAGATCCAGCAAGACCGGACCACTTTGACGGAAATAATGCTTCTCTGAAGACATAC 303
Db  1082 GAGGAGATCCAGCAAGACCGGACCACTTTGACGGAAATAATGCTTCTCTGAAGACATAC 1141

Qy  304 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 363
Db  1142 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 1201

Qy  364 GGCAATCAAGTTCTACCAAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTCAATCGGA 423
Db  1202 GGCAATCAAGTTCTACCAAGCGGTACGAATCGCTCAAGGAACATCGTTCCATTCAATCGGA 1261

Qy  424 TCCCTGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGC 483
Db  1262 TCCCTGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGC 1321

Qy  484 ACCAAGCTGAAGGATCTCTGCGCCAGCCCGGCCCAATTCGTCGCCAAGATCGACGTGGTC 543
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Qy  544 ATTTCCGAGGCGAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCACCTGCTTCGAA 603
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Db  1442 GACAGCGAATTTGGCCGATACCGTCAAGCCCAATTTCAACGCCAGCTTCCTCCATT 1501

Qy  664 CGTCAAGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCAAGACACAGAAAGTGAACCTAC 723
Db  1502 CGTCAAGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCAAGACACAGAAAGTGAACCTAC 1561

Qy  724 CTCATGACATGCTGCTTGGACACCATCTCCGACGACCGTTCGACACCAAGCTGTCC 783
Db  1562 CTCATGACATGCTGCTTGGACACCATCTCCGACGACCGTTCGACACCAAGCTGTCC 1621

Qy  784 CCCCTTCTGTGACCTGTTCAACCCATGACGAATGAGTCAACTACGACTACCTCCAGTCCCTTG 843
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Qy  844 AAAAAGTATTAACGGCATGTTGGTGAAGTAAACCCGCTCGGCCGACCCAGGGGTCGGGTAC 903
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Qy  964 CACACTTTGAGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTACGCGGACTTT 1023
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Db  1862 TCGCATGACACGCGCATCATCTCCATTCTCTTGTGTTAGCTCTGTACAACGCGCACTAAG 1921
Qy  1084 CCGCTATCTACCAACACCGTGGAGAAATATCAACCCAGACAGATGGAATTCCTGCTCTGG 1143
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Qy  1144 ACGGTTCCGTTTTCCTTCGCGTTTGTACGTTCAGATGATGCAAGTTCAGCGGCGAGCAGAG 1203
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Qy  1204 CCGCTGCTCCGCTGTCTTGGTTAATCATCGCTTGTCCCGCTGCATGGGTGTCGCGTTTGT 1263
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Qy  1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db  2102 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
Qy  1324 GGTGATTGGCGGAGTGTTCCTTAG 1350
Db  2162 GGTGATTGGCGGAGTGTTCCTTAG 2188
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RESULT 5
US-10-662-914-7
; Sequence 7, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingren
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H. J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-7

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 63
Db 842 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 901
Qy 64 TGCTTCTCCGAGACTTCGGCATCTTTGGGGTCAATPACACACCGTTCTTCTCTCTGGCAAAAC 123
Db 902 TGCTTCTCCGAGACTTCGGCATCTTTGGGGTCAATPACACACCGTTCTTCTCTCTGGCAAAAC 961
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Db 962 GAATCGGTCAATCTCCCTGAGGTGCCCGCGGATGCAGATCACTTCGCTCAGGTCCTC 1021
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Qy 244 GAGGAGATCCAGCAAGACCGGACCACTTTGACGGAAATAATGCTTCTCTGAAGACATAC 303
Db 1082 GAGGAGATCCAGCAAGACCGGACCACTTTGACGGAAATAATGCTTCTCTGAAGACATAC 1141

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Db 1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACGACCGTTCGACACCGAGCTGCC 1621
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Db 1622 CCTTCTGTGACCTGTTCAACCCATGACGAATGGATCAACTACGACTACCTCCAGTCTCTG 1681
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Db 1682 AAAAGATTATAGGCGATGTTGAGGTAACCGGCTCGCGCCGACCCAGGGGCTCGGTAC 1741
QY 904 GCTAACGAGCTCATCGCCGCTGTACCCACTGCTGTCCACGATGACACGAGTTCACAC 963
Db 1742 GCTAACGAGCTCATCGCCGCTGTACCCACTGCTGTCCACGATGACACGAGTTCACAC 1801
QY 964 CACACTTTGGACTGAGCGCGGTACCTTTCCGCTCACTCTCTCTACGCGGACTTT 1023
Db 1802 CACACTTTGGACTGAGCGCGGTACCTTTCCGCTCACTCTCTCTACGCGGACTTT 1861
QY 1024 TCGCATGACAAAGGATCATCTCCATTCTCTTTAGTCTGTGTAACAGGCACTAAG 1083
Db 1862 TCGCATGACAAAGGATCATCTCCATTCTCTTTAGTCTGTGTAACAGGCACTAAG 1921
QY 1084 CCGTATCTACACGACCGTGGAGAAATACCCAGACAGATGGAATCTCGTCTGTGTTG 1143
Db 1922 CCGTATCTACACGACCGTGGAGAAATACCCAGACAGATGGAATCTCGTCTGTGTTG 1981
QY 1144 ACGGTTCCGTTTGTCTCGGTTTCTAGTCGAGATGATGAGTGTACGGCGGAGCAGGAG 1203
Db 1982 ACGGTTCCGTTTGTCTCGGTTTCTAGTCGAGATGATGAGTGTACGGCGGAGCAGGAG 2041
QY 1204 CCGTGTGTCGTGTTGTTTAAATGATCGGCTGTCGCCGTTGATGAGGTTGTCGGGTTGAT 1263
Db 2042 CCGTGTGTCGTGTTGTTTAAATGATCGGCTGTCGCCGTTGATGAGGTTGTCGGGTTGAT 2101
QY 1264 GCTTTGGGAGATGATACCGGGATAGCTTTGTGAGGGGTTGAGCTTTGATAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGATACCGGGATAGCTTTGTGAGGGGTTGAGCTTTGATAGATCTGGG 1381
QY 1324 GGTGATTGGGCGGAGTGTGTTTGTCTAG 1350
Db 2162 GGTGATTGGGCGGAGTGTGTTTGTCTAG 2188
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RESULT 6
US-10-662-914-11
; Sequence 11, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullanev, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-11

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA 63
Db 842 CTGGCAGTCCCGCCTCGAGAAATCAATCCAGTTCGATACGGTTCGATCAGGGGTATCAA 901
QY 64 TGCTTCTCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTGTGCAAAAC 123
Db 902 TGCTTCTCGAGACTTCGCATCTTTGGGGTCTATACGACCGCTTCTTCTGTGCAAAAC 961
QY 124 GAATCGGTATCTCCCTCGAGTCCCGCGATACGAGTACGAGTTCGTCAGTCTCTC 183
Db 962 GAATCGGTATCTCCCTCGAGTCCCGCGATACGAGTACGAGTTCGTCAGTCTCTC 1021
QY 184 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCCGCTCTCAT 243
Db 1022 TCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCCGCTCTCAT 1081
QY 244 GAGGATCCAGACAGACGCGACCTTTGACGGAATATGCTTCTGAGACATAC 303
Db 1082 GAGGATCCAGACAGACGCGACCTTTGACGGAATATGCTTCTGAGACATAC 1141
QY 304 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 363
Db 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 1201
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Db 1202 GGCATCAAGTTCTACACGGGTACGAATCGTTCACAGGAACATCGTTCCATTCAATCCGA 1261
QY 424 TCCTCTGGCTCAGCGCGGTGATCCCTCCGGCAGAGAAATTCATCGAGGGTTCAGAGC 483
Db 1262 TCCTCTGGCTCAGCGCGGTGATCCCTCCGGCAGAGAAATTCATCGAGGGTTCAGAGC 1321
QY 484 ACCAAGCTGAAGATCTCTGTGCCAGCGCGGCAATCGTCCGCAAGAAATTCATCGAGGGTTCAGAGC 543
Db 1322 ACCAAGCTGAAGATCTCTGTGCCAGCGCGGCAATCGTCCGCAAGAAATTCATCGAGGGTTCAGAGC 1381
QY 544 ATTTCCGAGGCGAGCTCATPCCAACAACTCTCGACCCAGGCACTGCACTGTCTTCGAA 603
Db 1382 ATTTCCGAGGCGAGCTCATPCCAACAACTCTCGACCCAGGCACTGCACTGTCTTCGAA 1441
QY 604 GACAGCGAATTCGGCGATACCGTGCAGGCCAATTTCCACGCCACGTTGCTCCCTCCATT 663
Db 1442 GACAGCGAATTCGGCGATACCGTGCAGGCCAATTTCCACGCCACGTTGCTCCCTCCATT 1501
QY 664 CGTCAACGTCTGGAGACGACCTGTCGGTGTGACTCTCAAGACGACGAGTGCACCTAC 723
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Db 1502 CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAGTGACCTAC 1561
Qy 724 CTCATGGACATGTCTCTCTTCGACACCATCTCCACGACACCGTTCGACACCAAGCTGTCC 783
Db 1562 CTCATGGACATGTCTCTCTTCGACACCATCTCCACGACACCGTTCGACACCAAGCTGTCC 1621
Qy 784 CCCCTCTGTGACCTGTTCACCCATGACGATGAGATCACTACGACTACCTCCAGTCCCTTG 843
Db 1622 CCCCTCTGTGACCTGTTCACCCATGACGATGAGATCACTACGACTACCTCCAGTCCCTTG 1681
Qy 844 AAAAAGTATTACGGCCATGTGTGAGTAACCCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 903
Db 1682 AAAAAGTATTACGGCCATGTGTGAGTAACCCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 1741
Qy 904 GCTAACGAGCTCATCGCCGCTGTGACCCATGACGCTGTGCTGTGACGATGACACAGTTCCAAC 963
Db 1742 GCTAACGAGCTCATCGCCGCTGTGACCCATGACGCTGTGCTGTGACGATGACACAGTTCCAAC 1801
Qy 964 CACACTTTGGACTCGAGCCGGCTACCTTTCCGGCTCAACTCTACTCTCTACGGCGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCGGCTACCTTTCCGGCTCAACTCTACTCTCTACGGCGACTTT 1861
Qy 1024 TCGATGACAAACGGGATCATCTCATTTCTCTTTTCTTTAGTCTGTGTAAACGGGCACTAAG 1083
Db 1862 TCGATGACAAACGGGATCATCTCATTTCTCTTTTCTTTAGTCTGTGTAAACGGGCACTAAG 1921
Qy 1084 CCGCTACTACACGACCGTGGAGATATACCCAGACAGATGATCTGTCTGTCTGG 1143
Db 1922 CCGCTACTACACGACCGTGGAGATATACCCAGACAGATGATCTGTCTGTCTGG 1981
Qy 1144 ACGTTCGGTTTGTCTCGGTTTGTACGTGAGATGATGAGTGTGAGGCGGACGAG 1203
Db 1982 ACGTTCGGTTTGTCTCGGTTTGTACGTGAGATGATGAGTGTGAGGCGGACGAG 2041
Qy 1204 CCGTGTGCTGTGTCTGGTTTAAATGATCGGTTGTCCGGTGTGATGGTGTCCGGTTGAT 1263
Db 2042 CCGTGTGCTGTGTCTGGTTTAAATGATCGGTTGTCCGGTGTGATGGTGTCCGGTTGAT 2101
Qy 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 2161
Qy 1324 GGTGATTTGGCGGAGTGTCTTTGCTTTAG 1350
Db 2162 GGTGATTTGGCGGAGTGTCTTTGCTTTAG 2188

RESULT 7

US-10-662-914-17
; Sequence 17, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 17
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-17

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGGGAGTCCCGCTCGAGAAATCAATCCAGTTGGGATACGGTGCATCAGGGGTATCAA 53
Db 842 CTGGGAGTCCCGCTCGAGAAATCAATCCAGTTGGGATACGGTGCATCAGGGGTATCAA 901
Qy 64 TGTCTTCTCGAGACTTTCGCTCTTTGGGTTCAATACGACACCGTTCTTCTCTCTGGCAAA 123
Db 902 TGTCTTCTCGAGACTTTCGCTCTTTGGGTTCAATACGACACCGTTCTTCTCTCTGGCAAA 961
Qy 124 GAATCGGTCAATCTCCCTGAGTGTCCCGCGGATGAGAGTCACTTTGCTGAGGTCTTC 183
Db 962 GAATCGGTCAATCTCCCTGAGTGTCCCGCGGATGAGAGTCACTTTGCTGAGGTCTTC 1021
Qy 184 TCCCGTCAATGGAGCGGTTATCCGACCGACTCCAAAGGGCAAGAAATATCTCCGCTCTCAT 243
Db 1022 TCCCGTCAATGGAGCGGTTATCCGACCGACTCCGAGGGCAAGAAATATCTCCGCTCTCAT 1081
Qy 244 GAGGAGATCCAGCAGAACCGGACCACTTTGACGAAATATGCTTCTGTAAGACATAC 303
Db 1082 GAGGAGATCCAGCAGAACCGGACCACTTTGACGAAATATGCTTCTGTAAGACATAC 1141
Qy 304 AACTACAGCTTTGGTGCAGATGACCTGACTCCCTTCGGAGACAGAGCTAGTCAACTCC 363
Db 1142 AACTACAGCTTTGGTGCAGATGACCTGACTCCCTTCGGAGACAGAGCTAGTCAACTCC 1201
Qy 364 GGCATCAAGTCTTACCCAGCGGTACGAATCGCTCAACAAGGAAATCGTTCCATTTCATCG 423
Db 1202 GGCATCAAGTCTTACCCAGCGGTACGAATCGCTCAACAAGGAAATCGTTCCATTTCATCG 1261
Qy 424 TCTCTGGTCTCAGCCGCGTGTATCGGCTCCGGCAGAAATTCATCGAGGGCTTCAGAGC 483
Db 1262 TCTCTGGTCTCAGCCGCGTGTATCGGCTCCGGCAGAAATTCATCGAGGGCTTCAGAGC 1321
Qy 484 ACCAAGCTCAAGGATCTCTGTCGCCAGCCGCGCAATCGTCCGCCAAGATCCAGCTGGTC 543
Db 1322 ACCAAGCTCAAGGATCTCTGTCGCCAGCCGCGCAATCGTCCGCCAAGATCCAGCTGGTC 1381
Qy 544 ATTTCCGAGGCGAGCTCATCCAAACAACCTCTCGACCCAGGACCTGCACTCTCTCGAA 603
Db 1382 ATTTCCGAGGCGAGCTCATCCAAACAACCTCTCGACCCAGGACCTGCACTCTCTCGAA 1441
Qy 604 GACGCGAATTCGCGATACCGTTCGAAGCCAAATTTACCGCCACGTTGTCGCCCTCCATT 663
Db 1442 GACGCGAATTCGCGATACCGTTCGAAGCCAAATTTACCGCCACGTTGTCGCCCTCCATT 1501
Qy 664 CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAGTGACCTAC 723
Db 1502 CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAGTGACCTAC 1561
Qy 724 CTCATGGACATGTCTCTCTTCGACACCATCTCCACGACCGCTGCACACCGAGCTGCC 783
Db 1562 CTCATGGACATGTCTCTCTTCGACACCATCTCCACGACCGCTGCACACCGAGCTGCC 1621
Qy 784 CCTTCTGTGACTGTTCACCCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 843
Db 1622 CCTTCTGTGACTGTTCACCCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 1681
Qy 844 AAAAGTATTACGGCCATGTTGACGATACCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 903
Db 1682 AAAAGTATTACGGCCATGTTGACGATACCGCTCGGCCCGACCCAGGGCGTCCGGCTAC 1741
Qy 904 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTCCAGATGACACAGTTCCAAC 963
Db 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCTGTCCAGATGACACAGTTCCAAC 1801
Qy 964 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1861
Qy 1024 TCGCATGACAAACGGGATCATCTCTCTTTGTTAGGTCTGTAGAACGGGCACTAAG 1083
Db 1862 TCGCATGACAAACGGGATCATCTCTCTTTGTTAGGTCTGTAGAACGGGCACTAAG 1921
Qy 1084 CCGCTATCTACCAACGACCGTGGAGAAATATCAACCCAGACAGATGATCTGTCTGTCTGG 1143

Db	1222	CCGCTATCTACCGACCGTGGAGATATCACCCAGACAGATGATTCTCGTCTGCTTGG	1581
Qy	1144	ACGGTTCGCTTTGCTTCGCTTTGTACGTCGAGATGATGCAAGTGTCAAGCGGAGCAGGAG	1203
Db	1982	ACGGTTCGCTTTGCTTCGCTTTGTACGTCGAGATGATGCAAGTGTCAAGCGGAGCAGGAG	2041
Qy	1204	CCGCTGTCGCTGTCCTTGGTTAATGATCGCGTGTGCCGCTGCATCGGTCGCGTTGAT	1563
Db	2042	CCGCTGTCGCTGTCCTTGGTTAATGATCGCGTGTGCCGCTGCATCGGTCGCGTTGAT	2101
Qy	1264	GCCTTGGGAGATGTACCCGGAGATGCTTTGTCAGGGGGTTGAGCTTTGCTAGATCTGGG	1323
Db	2102	GCCTTGGGAGATGTACCCGGAGATGCTTTGTCAGGGGGTTGAGCTTTGCTAGATCTGGG	2161
Qy	1324	GGTGATTGGCGGAGTGTTTTGCTTAG	1350
Db	2162	GGTGATTGGCGGAGTGTTTTGCTTAG	2188

RESULT 8

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1  RESULT 8
2  US-10-662-914-19
3  ; Sequence 19, Application US/10662914
4  ; Publication No. US20040126844A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Lei, Xingen
7  ; APPLICANT: Mullaney, Edward J
8  ; APPLICANT: Ullah, Abul H.J.
9  ; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
10 ;
11 ; FILE REFERENCE: 19603/4261
12 ; CURRENT APPLICATION NUMBER: US/10/662,914
13 ; CURRENT FILING DATE: 2003-09-15
14 ; PRIOR APPLICATION NUMBER: 60/410,736
15 ; PRIOR FILING DATE: 2002-09-13
16 ; NUMBER OF SEQ ID NOS: 69
17 ; SOFTWARE: PatentIn Ver. 2.1
18 ; SEQ ID NO 19
19 ; LENGTH: 2665
20 ; TYPE: DNA
21 ; ORGANISM: Aspergillus niger
22 US-10-662-914-19

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RESULT 9
US-10-662-914-21
; Sequence 21, Application US/10662914
; Publication No. US20040126944A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J

```

Qy	424	TCTCTGGCTCCAGCCGCGTGTATCGCCTCGGCAAGAAATTCATCGAGGCTTCCAGAC	483
Db	1262	TCTCTGGCTCCAGCCGCGTGTATCGCCTCGGCAAGAAATTCATCGAGGCTTCCAGAC	1321
Qy	484	ACCAAGCTAAGGATCCTCGTGCACGACGCGGCAATCGTGCGCCAAGATCGACGTGTGC	543
Db	1322	ACCAAGCTAAGGATCCTCGTGCACGACGCGGCAATCGTGCGCCAAGATCGACGTGTGC	1381
Qy	544	ATTTCCGAGCCAGCTATCCAAACAATCTCGAGCCAGGCACTGTGACTGTCTTCGAA	603
Db	1382	ATTTCCGAGCCAGCTATCCAAACAATCTCGAGCCAGGCACTGTGACTGTCTTCGAA	1441
Qy	604	GACAGCGAATTGGCCGATACCGTGCAGAGCAATTTCAACGCCACAGTTTCGTCCTCCATT	663
Db	1442	GACAGCGAATTGGCCGATACCGTGCAGAGCAATTTCAACGCCACAGTTTCGTCCTCCATT	1501
Qy	664	CGTCAACGCTCGAGAAACAACCTGTCGGTGTGACTCTCACAGACACAGAAGTGACCTAC	723
Db	1502	CGTCAACGCTCGAGAAACAACCTGTCGGTGTGACTCTCACAGACACAGAAGTGACCTAC	1561
Qy	724	CTCATCGCATGTGCTCTTCGACACCACTCTCCACAGCACCGTCGACACCAAGCTGCC	783
Db	1562	CTCATCGCATGTGCTCTTCGACACCACTCTCCACAGCACCGTCGACACCAAGCTGCC	1621
Qy	784	CCCTTCTGTGACCTGTTACCCATGACGAATGGATCAACTACGACTACTCTCCAGTCTCTG	843
Db	1622	CCCTTCTGTGACCTGTTACCCATGACGAATGGATCAACTACGACTACTCTCCAGTCTCTG	1681
Qy	844	AAAAGTATTACGGCCATGGTCAGGTACCCGCTCGGCCGACCCAGCGCTCGGCTAC	903
Db	1682	AAAAGTATTACGGCCATGGTCAGGTACCCGCTCGGCCGACCCAGCGCTCGGCTAC	1741
Qy	904	GTTAACGAGCTCATCCCGCTGTGACCCACTCGCCTGTCCAGATGACACCAAGTTCACAC	963
Db	1742	GTTAACGAGCTCATCCCGCTGTGACCCACTCGCCTGTCCAGATGACACCAAGTTCACAC	1801
Qy	964	CACACTTTGGACTCGAGCCGGGTACTCTTTCGCTCAACTCTACTCTCTACCGGACITTT	1023
Db	1802	CACACTTTGGACTCGAGCCGGGTACTCTTTCGCTCAACTCTACTCTCTACCGGACITTT	1861
Qy	1024	TGCGATGACAAAGGCAATCATCTCCATTCTCTTTGGTTTAGTCTGTACAAAGGCACTAAG	1083
Db	1862	TGCGATGACAAAGGCAATCATCTCCATTCTCTTTGGTTTAGTCTGTACAAAGGCACTAAG	1921
Qy	1084	CGGCTATACCAAGCAGCGTGAGAAATACACCGACAGATGGATTTCTCTGCTGCTGG	1143
Db	1922	CGGCTATACCAAGCAGCGTGAGAAATACACCGACAGATGGATTTCTCTGCTGCTGG	1981
Qy	1144	ACGGTTCCGTTTGTCTTCGGTTTGTACGTCGAGATGATGCACTGTTCAGCGGAGCAGGAG	1203
Db	1982	ACGGTTCCGTTTGTCTTCGGTTTGTACGTCGAGATGATGCACTGTTCAGCGGAGCAGGAG	2041
Qy	1204	CCGCTGGTCCGTTGTCTTGGTTTAATGATCGCGTTTCCCGCTGCATGGGTTCCGGTTGAT	1263
Db	2042	CCGCTGGTCCGTTGTCTTGGTTTAATGATCGCGTTTCCCGCTGCATGGGTTCCGGTTGAT	2101
Qy	1264	GTTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTTCAGCTTCTAGATCTGGG	1323
Db	2102	GTTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTTCAGCTTCTAGATCTGGG	2161
Qy	1324	GGTGAATTGGCGGAGTGTCTTCTCTAG	1350
Db	2162	GGTGAATTGGCGGAGTGTCTTCTCTAG	2188

RESULT 9
US-10-662
; Sequenc
; Publica
; GENERAI
; APPLIC
; APPLIC

APPLICANT: Ullah, Abul H. J.
TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
FILE REFERENCE: 19603/4261
CURRENT APPLICATION NUMBER: US/10/662,914
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: 60/410,736
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 2665
TYPE: DNA
ORGANISM: Aspergillus niger
US-10-662-914-21

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 63
DB 842 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 901

QY 64 TGCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 123
DB 902 TGCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 961

QY 124 GAATCGGTGATCTCCCTGAGGTGCCCGCGGATGACAGTCACTTTCGTCAGGTCCTC 183
DB 962 GAATCGGTGATCTCCCTGAGGTGCCCGCGGATGACAGTCACTTTCGTCAGGTCCTC 1021

QY 184 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGCAAGAAATACCTCCGCTCATTT 243
DB 1022 TCCCGTCATGAGCGGGTATCCGACCGACTCCAAAGGCAAGAAATACCTCCGCTCATTT 1081

QY 244 GAGGAGATCCAGACAGCGGACCACTTTGACGGAATATGCTTCCTGAAGACATAC 303
DB 1082 GAGGAGATCCAGACAGCGGACCACTTTGACGGAATATGCTTCCTGAAGACATAC 1141

QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGGTAGTCAACTCG 363
DB 1142 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGGAGAACAGAGGTAGTCAACTCG 1201

QY 364 GGATCAAGTTTACACGAGGTACGATCGCTCACAGGAACATCGTTCATTCATCCGA 423
DB 1202 GGATCAAGTTTACACGAGGTACGATCGCTCACAGGAACATCGTTCATTCATCCGA 1261

QY 424 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCAAGAAATTCATCGAGGCTTCAGAGC 483
DB 1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCAAGAAATTCATCGAGGCTTCAGAGC 1321

QY 484 ACCAAGTGAAGATCCTCTGCCCCAGCCCGGCAATCGTCCGCAAGATCGACGTGGTC 543
DB 1322 ACCAAGTGAAGATCCTCTGCCCCAGCCCGGCAATCGTCCGCAAGATCGACGTGGTC 1381

QY 544 ATTTCCGAGCCAGCTCATCCACAACTCTCGACCCAGGACCTGCACTGTCTCGAA 603
DB 1382 ATTTCCGAGCCAGCTCATCCACAACTCTCGACCCAGGACCTGCACTGTCTCGAA 1441

QY 604 GACAGCAATTTGGCCGATACCGTCGAAGCCAAATTTACCGCCCAAGTTTCGTCCTCCATT 663
DB 1442 GACAGCAATTTGGCCGATACCGTCGAAGCCAAATTTACCGCCCAAGTTTCGTCCTCCATT 1501

QY 664 CHTCAAGCTTGAGAACGACCTGTGCGGTGACTCTCACAGACACAGAGTGACCTAC 723
DB 1502 CHTCAAGCTTGAGAACGACCTGTGCGGTGACTCTCACAGACACAGAGTGACCTAC 1561

QY 724 CTCATGACATGTCTCTTCGACACCATCTCCACAGACCGTTCGACACCAAGCTGTCC 783
DB 1562 CTCATGACATGTCTCTTCGACACCATCTCCACAGACCGTTCGACACCAAGCTGTCC 1621

QY 784 CCCTCTGTGACCTGTTCACCCATGAGATCAATACGATCACTTCAGTCTCCAGTCTTTG 843

DB 1622 CCCTTCTGTGACCTGTTCAACCATGCAAGATGGATCAACTAGCACTACTCCTCAGTCTTGG 1681
QY 844 AAAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCGGACCCAGGGGTCTGGCTAC 903
DB 1682 AAAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCGGACCCAGGGGTCTGGCTAC 1741

QY 904 GCTAACGAGCTCATCGCCGCTGACCCACCTGACCTGCTGCTCCAGATGACACCAAGTTCAC 963
DB 1742 GCTAACGAGCTCATCGCCGCTGACCCACCTGACCTGCTGCTCCAGATGACACCAAGTTCAC 1801

QY 964 CACACTTTGGACTCGAGCCCGGCTACCTTTCGCTCAACTCTACTCTCTAGCGGACTTT 1023
DB 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCGCTCAACTCTACTCTCTAGCGGACTTT 1861

QY 1024 TCGATGACACGGGATCATCTCCATTTCTTTGGTTAGTCTGTACAAACGGCACTAAG 1083
DB 1862 TCGATGACACGGGATCATCTCCATTTCTTTGGTTAGTCTGTACAAACGGCACTAAG 1921

QY 1084 CCGCTATCTACCAACACCGTGGAGATATCAACCCAGACAGATGGATTCCTGCTGCTTGG 1143
DB 1922 CCGCTATCTACCAACACCGTGGAGATATCAACCCAGACAGATGGATTCCTGCTGCTTGG 1981

QY 1144 ACGTTCCGTTTTCGCTGCTTGTGATGTCAGATGATGTCAGGCGGAGCAGAG 1203
DB 1982 ACGTTCCGTTTTCGCTGCTTGTGATGTCAGATGATGTCAGGCGGAGCAGAG 2041

QY 1204 CCGCTGGTCCGCTGCTTAAATGATCGCTGTCGCGTGCATGGGTGTCGCTTGG 1263
DB 2042 CCGCTGGTCCGCTGCTTAAATGATCGCTGTCGCGTGCATGGGTGTCGCTTGG 2101

QY 1264 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 1323
DB 2102 GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 2161

QY 1324 GGTGATTCGGCGGAGTGTTCCTTAG 1350
DB 2162 GGTGATTCGGCGGAGTGTTCCTTAG 2188

RESULT 10

US-10-662-914-23
Sequence 23, Application US/10662914
Publication No. US20040128844A1
GENERAL INFORMATION:
APPLICANT: Lei, Xingen
APPLICANT: Mullaney, Edward J.
APPLICANT: Ullah, Abul H. J.
TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
FILE REFERENCE: 19603/4261
CURRENT APPLICATION NUMBER: US/10/662,914
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: 60/410,736
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 2665
TYPE: DNA
ORGANISM: Aspergillus niger
US-10-662-914-23

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 63
DB 842 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGGATACGGTTCGATCAGGGGTATCAA 901
QY 64 TGCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 123
DB 902 TGCTTCTCCGAGACTTCGATCTTTGGGGTCAATACGACCGTTCCTCTCTGGCAAC 961

124 GAATCGGTGATCTCCCTGAGTCCCGCGGATGACAGAGTCATCTTTCGCTCAGGTCTC 183
Db
962 GAATCGGTGATCTCCCTGAGTCCCGCGGATGACAGAGTCATCTTTCGCTCAGGTCTC 1021
Qy
184 TCCCGTATGAGCGCGGTATCCGACGATCTCAAGGGGAAAGAAATCTCGCTCTCAT 243
Db
1022 TCCCGTATGAGCGCGGTATCCGACGATCTCAAGGGGAAAGAAATCTCGCTCTCAT 1081
Qy
244 GAGGAGATCCAGCAGAGACGCGACCATCTTTGACGGAATAATGCTTCCTGGAAGACATAC 303
Db
1082 GAGGAGATCCAGCAGAGACGCGACCATCTTTGACGGAATAATGCTTCCTGGAAGACATAC 1141
Qy
304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAAACAGGAGCTAGTCAACTCC 363
Db
1142 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAAACAGGAGCTAGTCAACTCC 1201
Qy
364 GGCATCAAGTTCACCGCGGTACGAATCGCTCAAGGGAACATCGTTCCATTCATCCGA 423
Db
1202 GGCATCAAGTTCACCGCGGTACGAATCGCTCAAGGGAACATCGTTCCATTCATCCGA 1261
Qy
424 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCGAAGAAATTCATCGAGGCTTCCAGAGC 483
Db
1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCGAAGAAATTCATCGAGGCTTCCAGAGC 1321
Qy
484 ACCAAGCTGAAGGATCTCGTCCGACGCGCGCAATCGTCGCCCAAGATCGACGTGGTC 543
Db
1322 ACCAAGCTGAAGGATCTCGTCCGACGCGCGCAATCGTCGCCCAAGATCGACGTGGTC 1381
Qy
544 ATTTCCGAGGCGAGCTATCCAAACACACTCTGACCCAGGACCTGCACTGCTTCGAA 603
Db
1382 ATTTCCGAGGCGAGCTATCCAAACACACTCTGACCCAGGACCTGCACTGCTTCGAA 1441
Qy
604 GACAGCGAATTTGGCGATACCGTCCGAGGCAATTTACCGCCAGCTTCGCTCCCTCAT 663
Db
1442 GACAGCGAATTTGGCGATACCGTCCGAGGCAATTTACCGCCAGCTTCGCTCCCTCAT 1501
Qy
664 CGTCAAGCTCGGAGACGACCTGTCGGGTGACTCTCAAGACACAGAAATGACCTAC 723
Db
1502 CGTCAAGCTCGGAGACGACCTGTCGGGTGACTCTCAAGACACAGAAATGACCTAC 1561
Qy
724 CTCATGACATGTGCTCTCGACACCATCTCCAGGACCGTTCGACACAGAGCTGTCC 783
Db
1562 CTCATGACATGTGCTCTCGACACCATCTCCAGGACCGTTCGACACAGAGCTGTCC 1621
Qy
784 CCCTTCGTGACCTGTTCAACCATGACGAATGGAATCAACTACGATCACTCCAGTCTTG 843
Db
1622 CCCTTCGTGACCTGTTCAACCATGACGAATGGAATCAACTACGATCACTCCAGTCTTG 1681
Qy
844 AAAAGTATTACGGCCATGTTGACAGGTAAACCGCTCGGCGCGACCCAGGCGGTGGGTAC 903
Db
1682 AAAAGTATTACGGCCATGTTGACAGGTAAACCGCTCGGCGCGACCCAGGCGGTGGGTAC 1741
Qy
904 GCTAACAGAGCTATCGCCCGCTGACCCACTCGCGGTGTCACGATGACACAGGTTCCAC 963
Db
1742 GCTAACAGAGCTATCGCCCGCTGACCCACTCGCGGTGTCACGATGACACAGGTTCCAC 1801
Qy
964 CACACTTTGGACTCGAGCGCGGTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db
1802 CACACTTTGGACTCGAGCGCGGTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1861
Qy
1024 TCGATGACACAGGATCATCTCCATTTCTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 1083
Db
1862 TCGATGACACAGGATCATCTCCATTTCTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 1921
Qy
1084 CGGCTATCTACACGACCGTGGAGAAATACCCAGACAGATGATTTCTCGTCTGCTTG 1143
Db
1922 CGGCTATCTACACGACCGTGGAGAAATACCCAGACAGATGATTTCTCGTCTGCTTG 1981
Qy
1144 ACGGTTCCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 1203
Db
1982 ACGGTTCCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 2041
Qy
1204 CCGCTGTCCTGTTTAAATGATCGCTGTTGTCGCTGTCATGGGTGTCCTCGGTTGAT 1263

RESULT 11

US-10-662-914-25
; Sequence 25, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H J
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-25

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTTCGATAGCGTCGATCAGGGGTATCAA 63
Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTTCGATAGCGTCGATCAGGGGTATCAA 901
QY 64 TGCCTTCGAGACTTCGCACTTTGGGGTCAATACGACCGTTCTTCTCTGCGCAAC 123
Db 902 TGCCTTCGAGACTTCGCACTTTGGGGTCAATACGACCGTTCTTCTCTGCGCAAC 961
QY 124 GAATCGGTATCTCCCTGAGTGCGCCCGGATCGAGTCACTTTTCGCTCAGGTCTCTC 183
Db 962 GAATCGGTATCTCCCTGAGTGCGCCCGGATCGAGTCACTTTTCGCTCAGGTCTCTC 1021
QY 184 TCCCGTATGAGCGGTATCCGACCGATCTCCAAAGGCAAGAAATATCTCGCTCTCAT 243
Db 1022 TCCCGTATGAGCGGTATCCGACCGATCTCCAAAGGCAAGAAATATCTCGCTCTCAT 1081
QY 244 GAGGAGATCCAGCAGAGACGCGACCATCTTGACGGAATAATGCTTCCTGGAAGACATAC 303
Db 1082 GAGGAGATCCAGCAGAGACGCGACCATCTTGACGGAATAATGCTTCCTGGAAGACATAC 1141
QY 304 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAAACAGGAGCTAGTCAACTCC 363
Db 1142 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGAAACAGGAGCTAGTCAACTCC 1201
QY 364 GGCATCAAGTTCACCGCGGTACGAATCGCTCAAGGGAACATCGTTCCATTCATCCGA 423
Db 1202 GGCATCAAGTTCACCGCGGTACGAATCGCTCAAGGGAACATCGTTCCATTCATCCGA 1261
QY 424 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCGAAGAAATTCATCGAGGCTTCCAGAGC 483
Db 1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGCGAAGAAATTCATCGAGGCTTCCAGAGC 1321
QY 484 ACCAAGCTGAAGGATCTCGTCCGACGCGCGCAATCGTCCCGCAAGATGACGTGGTC 543
Db 1322 ACCAAGCTGAAGGATCTCGTCCGACGCGCGCAATCGTCCCGCAAGATGACGTGGTC 1381

QY 544 ATTTCCGAGGCGAGCTCATCCAAACAACACTCTCGACCCAGGCACTCGACTGCTTCGAA 603
Db |||||
QY 1382 ATTTCCGAGGCGAGCTCATCCAAACAACACTCTCGACCCAGGCACTCGACTGCTTCGAA 1441
Db |||||
QY 604 GACAGCGAATTGGCGGATACCGTCCGAAGCCAAATTTACCGCCAGCTTCGTCCTCCATT 663
Db |||||
QY 1442 GACAGCGAATTGGCGGATACCGTCCGAAGCCAAATTTACCGCCAGCTTCGTCCTCCATT 1501
Db |||||
QY 664 CGTCAAGCTTGGAGAACGACCTCTCGCGGTGATCTCTCACAGACACAGAAGTGACCTAC 723
Db |||||
QY 1502 CGTCAAGCTTGGAGAACGACCTCTCGCGGTGATCTCTCACAGACACAGAAGTGACCTAC 1561
Db |||||
QY 724 CTCATGACATGCTCTCTTCGACACCATCTCCACAGCACCCTCGACACCAAGCTGTC 783
Db |||||
QY 1562 CTCATGACATGCTCTCTTCGACACCATCTCCACAGCACCCTCGACACCAAGCTGTC 1621
Db |||||
QY 784 CCCTTCTGTGACCTGTTTCAACCATGAGCAATGAGTCAACTACGACTACTCTCCAGTCTCTG 843
Db |||||
QY 1622 CCCTTCTGTGACCTGTTTCAACCATGAGCAATGAGTCAACTACGACTACTCTCCAGTCTCTG 1681
Db |||||
QY 844 AAAAAGTATTAGGCGCATGTTGCGAGGTAAACCGCTCGGCCGAGCCAGGGCGTCGGCTAC 903
Db |||||
QY 1682 AAAAAGTATTAGGCGCATGTTGCGAGGTAAACCGCTCGGCCGAGCCAGGGCGTCGGCTAC 1741
Db |||||
QY 904 GCTAACGAGCTCATCGCCCGCTGTGACCCACTCGCTGTGCACGATGACACAGTTCCTAAC 963
Db |||||
QY 1742 GCTAACGAGCTCATCGCCCGCTGTGACCCACTCGCTGTGCACGATGACACAGTTCCTAAC 1801
Db |||||
QY 964 CACACTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
Db |||||
QY 1802 CACACTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1861
Db |||||
QY 1024 TCGCATCAGACGSCATCACTCTCATCTCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 1083
Db |||||
QY 1862 TCGCATCAGACGSCATCACTCTCATCTCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 1921
Db |||||
QY 1084 CCGTATCTACACGACCGTGGAGATATCACCCAGACAGATGAGTCTCTGCTGCTTG 1143
Db |||||
QY 1922 CCGTATCTACACGACCGTGGAGATATCACCCAGACAGATGAGTCTCTGCTGCTTG 1981
Db |||||
QY 1144 ACGGTTCCGTTTGGTTTGGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 1203
Db |||||
QY 1982 ACGGTTCCGTTTGGTTTGGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 2041
Db |||||
QY 1204 CCGTGTCTCGCTGCTTCTGTTTAAATGATCGGCTGCTCCGCTGATGGGTGCTCCGTTGAT 1263
Db |||||
QY 2042 CCGTGTCTCGCTGCTTCTGTTTAAATGATCGGCTGCTCCGCTGATGGGTGCTCCGTTGAT 2101
Db |||||
QY 1264 GCTTTGGGAGATGATACCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db |||||
QY 2102 GCTTTGGGAGATGATACCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
Db |||||
QY 1324 GGTGATTGGCGGAGTCTTTGCTTAG 1350
Db |||||
QY 2162 GGTGATTGGCGGAGTCTTTGCTTAG 2188
Db |||||

RESULT 12

US-10-662-914-27
; Sequence 27, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-27

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTCGGATACCGTTCAGTACAGGGGTATCAA 63
Db |||||
QY 842 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTCGGATACCGTTCAGTACAGGGGTATCAA 901
Db |||||
QY 64 TGCTTCTCGAGACTTCGCAATCTTTGGGTCAATACGACCCGTTCTTCTCTCTGCGCAAC 123
Db |||||
QY 902 TGCTTCTCGAGACTTCGCAATCTTTGGGTCAATACGACCCGTTCTTCTCTCTGCGCAAC 961
Db |||||
QY 124 GAATCGGTATCTCCCTGAGTGCCCGCGGATCGAGTCACTTTGCTGCTGAGTCTCTC 183
Db |||||
QY 962 GAATCGGTATCTCCCTGAGTGCCCGCGGATCGAGTCACTTTGCTGCTGAGTCTCTC 1021
Db |||||
QY 184 TCCGCTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 243
Db |||||
QY 1022 TCCGCTCATGAGCGCGGTATCCGACCGACTCCAAAGGCAAGAAATATCTCCGCTCTCAT 1081
Db |||||
QY 244 GAGGAGATCCAGCAAGAACCGGACCACTTTGACGAAATATGCTTCTGAGACATAC 303
Db |||||
QY 1082 GAGGAGATCCAGCAAGAACCGGACCACTTTGACGAAATATGCTTCTGAGACATAC 1141
Db |||||
QY 304 AACTACAGTTTGGGTGAGATGACCTGCTCCCTCGGACAGGAGCTAGTCACTCC 363
Db |||||
QY 1142 AACTACAGTTTGGGTGAGATGACCTGCTCCCTCGGACAGGAGCTAGTCACTCC 1201
Db |||||
QY 364 GGCATCAAGTTTACACAGCGGTACGAATCGCTCAACAGAAACATCGTTTCCATTCATCG 423
Db |||||
QY 1202 GGCATCAAGTTTACACAGCGGTACGAATCGCTCAACAGAAACATCGTTTCCATTCATCG 1261
Db |||||
QY 424 TCCTCTGGCTCCAGCGGCTGATCGCTCCGCAAGAAATTCATCGAGGGCTTCAGAGC 483
Db |||||
QY 1262 TCCTCTGGCTCCAGCGGCTGATCGCTCCGCAAGAAATTCATCGAGGGCTTCAGAGC 1321
Db |||||
QY 484 ACCAAGCTGAAGAGTCTCTGTCGCCAGCCCGCCCAATCGTCCGCCAAGATCGACGTGTC 543
Db |||||
QY 1322 ACCAAGCTGAAGAGTCTCTGTCGCCAGCCCGCCCAATCGTCCGCCAAGATCGACGTGTC 1381
Db |||||
QY 544 ATTTCCGAGGCGAGCTCATCAAACAACCTCTGACCCAGGCACTGCACTGTCTTCGAA 603
Db |||||
QY 1382 ATTTCCGAGGCGAGCTCATCAAACAACCTCTGACCCAGGCACTGCACTGTCTTCGAA 1441
Db |||||
QY 604 GACAGCGAATTGGCGGATACCGTCCGAAGCCAAATTTACCGCCAGCTTCGTCCTCCATT 663
Db |||||
QY 1442 GACAGCGAATTGGCGGATACCGTCCGAAGCCAAATTTACCGCCAGCTTCGTCCTCCATT 1501
Db |||||
QY 664 GGTCAACGTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTAC 723
Db |||||
QY 1502 GGTCAACGTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTAC 1561
Db |||||
QY 724 CTCATGACATGCTCTCTTCGACACCATCTCCACAGCACCCTCGACACCAAGCTGTC 783
Db |||||
QY 1562 CTCATGACATGCTCTCTTCGACACCATCTCCACAGCACCCTCGACACCAAGCTGTC 1621
Db |||||
QY 784 CCCTTCTGTGACCTGTTTCAACCATGAGCAATGAGTCAACTACGACTACTCTCCAGTCTCTG 843
Db |||||
QY 1622 CCCTTCTGTGACCTGTTTCAACCATGAGCAATGAGTCAACTACGACTACTCTCCAGTCTCTG 1681
Db |||||
QY 844 AAAAAGTATTAGGCGCATGTTGCGAGGTAAACCGCTCGGCCGAGCCAGGGCGTCGGCTAC 903
Db |||||
QY 1682 AAAAAGTATTAGGCGCATGTTGCGAGGTAAACCGCTCGGCCGAGCCAGGGCGTCGGCTAC 1741
Db |||||
QY 904 GCTAACGAGCTCATCGCCCGCTGTGACCCACTCGCTGTGCACGATGACACAGTTCCTAAC 963
Db |||||

Db 1742 GCTAAAGAGCTCATGCGCGCTCTGACCCACTCGCTGTCTCCAGATGACACCACTTCCAAAC 1801
QY 964 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1861
QY 1024 TCGCATGACAAAGCGCATCATCTCCATTCTCTTTAGGTGTGACAAAGCGCACTAAG 1083
Db 1862 TCGCATGACAAAGCGCATCATCTCCATTCTCTTTAGGTGTGACAAAGCGCACTAAG 1921
QY 1084 CCGTATCTACCAAGCGGTGGAGAAATCACCCAGACAGATGGATCTCGTCTGCTTGG 1143
Db 1922 CCGTATCTACCAAGCGGTGGAGAAATCACCCAGACAGATGGATCTCGTCTGCTTGG 1981
QY 1144 ACGGTTCCGTTTGTCTCGCGCTTTGTACGTGAGATGATGACGTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1203
Db 1982 ACGGTTCCGTTTGTCTCGCGCTTTGTACGTGAGATGATGACGTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 2041
QY 1204 CCGTGTGCTGCTGCTTGGTTAATGATCGGTTGTCCGCTGCAATGGGTGCTCGGTTGAT 1263
Db 2042 CCGTGTGCTGCTGCTTGGTTAATGATCGGTTGTCCGCTGCAATGGGTGCTCGGTTGAT 2101
QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY 1324 GGTGATTGGGCGGAGTGTGTTGCTTAG 1350
Db 2162 GGTGATTGGGCGGAGTGTGTTGCTTAG 2188

RESULT 13
US-10-662-914-29
; Sequence 29, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 29
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-29

Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGGCATACGGTTCGATCAGGGGTATCAA 63
Db 842 CTGGCAGTCCCGGCTCGAGAAATCAATCCAGTTGGCATACGGTTCGATCAGGGGTATCAA 901
QY 64 TGCTTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGCAACGGTTCCTCTCTCGGCAAC 123
Db 902 TGCTTCTCCGAGACTTCGCAATCTTTGGGGTCAATACGCAACGGTTCCTCTCTCGGCAAC 961
QY 124 GAATCGGTCATCTCCCTGAGTGCCTCGCGGATGCGAGTCACTTTGCTCAGGTCCTC 183
Db 962 GAATCGGTCATCTCCCTGAGTGCCTCGCGGATGCGAGTCACTTTGCTCAGGTCCTC 1021
QY 184 TCCGCTCATGAGCGCGGTATCCGACCGACTTCCAAAGGCAAGAAATCTCCGCTCTCAT 243
Db 1022 TCCGCTCATGAGCGCGGTATCCGACCGACTTCCAAAGGCAAGAAATCTCCGCTCTCAT 1081

QY 244 GAGGAGATCCAGCAGAACCGACCACTTTGACCGAAATATGCTTCTTGAAGACATAC 303
Db 1082 GAGGAGATCCAGCAGAACCGACCACTTTGACCGAAATATGCTTCTTGAAGACATAC 1141
QY 304 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGGAGAAACAGGAGTAGTCAACTCC 363
Db 1142 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGGAGAAACAGGAGTAGTCAACTCC 1201
QY 364 GGCATCAAGTTCTACAGCGGTACGAATCGTCTCAAGGAACATCGTTCATTCATCGGA 423
Db 1202 GGCATCAAGTTCTACAGCGGTACGAATCGTCTCAAGGAACATCGTTCATTCATCGGA 1261
QY 424 TCCCTGTGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGGTTCCAGAGC 483
Db 1262 TCCCTGTGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGGTTCCAGAGC 1321
QY 484 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGCAATGCTGCCCAAGATCGAGTGGTC 543
Db 1322 ACCAAGCTGAAGGATCTCTGTCGCCAGCCCGCAATGCTGCCCAAGATCGAGTGGTC 1381
QY 544 ATTTCCGAGGCGAGTCAATCCAAACAACACTCTCGACCCAGGCACTGCACTGTCTCGAA 603
Db 1382 ATTTCCGAGGCGAGTCAATCCAAACAACACTCTCGACCCAGGCACTGCACTGTCTCGAA 1441
QY 604 GACACGGAATTTGGCGGATACCGTTCGAAGCCAAATTTCAACGCCAGTTCGTCCTCAATT 663
Db 1442 GACACGGAATTTGGCGGATACCGTTCGAAGCCAAATTTCAACGCCAGTTCGTCCTCAATT 1501
QY 664 CGTCAACGCTGAGAACAGACTGTCGGGTGTGACTCTCAGACACAGACAGTGCACCTAC 723
Db 1502 CGTCAACGCTGAGAACAGACTGTCGGGTGTGACTCTCAGACACAGACAGTGCACCTAC 1561
QY 724 CTCATGGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTCGACACCAAGCTGTC 783
Db 1562 CTCATGGACATGTGCTCTCTCGACACCATCTCCACAGCACCGTCGACACCAAGCTGTC 1621
QY 784 CCGTTCTGTGACCTGTTTCAACCATGACGAATGGATCAACTAGACTACCTCCAGTCCCTG 843
Db 1622 CCGTTCTGTGACCTGTTTCAACCATGACGAATGGATCAACTAGACTACCTCCAGTCCCTG 1681
QY 844 AAAAAGTATTAGGCGCATGTGCGAGTAAACCGCTCGGCCCGACCCAGGGGCTCGGCTAC 903
Db 1682 ACAAAGTATTAGGCGCATGTGCGAGTAAACCGCTCGGCCCGACCCAGGGGCTCGGCTAC 1741
QY 904 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCCTGTCCAGATGACACAGTTCACAC 963
Db 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCCTGTCCAGATGACACAGTTCACAC 1801
QY 964 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1023
Db 1802 CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1861
QY 1024 TCGCATGACAAAGCGCATCATCTCCATTCTTTGCTTTAGTCTGTGACAAAGCGCACTAAG 1083
Db 1862 TCGCATGACAAAGCGCATCATCTCCATTCTTTGCTTTAGTCTGTGACAAAGCGCACTAAG 1921
QY 1084 CCGCTATCTACACAGCGTGGAGAAATCACCCAGACAGATGGATCTCTGCTGCTTGG 1143
Db 1922 CCGCTATCTACACAGCGTGGAGAAATCACCCAGACAGATGGATCTCTGCTGCTTGG 1981
QY 1144 ACGGTTCCGTTTGTCTCGCGCTTTGTACGTGAGATGATGACGTGTGAGGGGGTTCAGGCGAGGAG 1203
Db 1982 ACGGTTCCGTTTGTCTCGCGCTTTGTACGTGAGATGATGACGTGTGAGGGGGTTCAGGCGAGGAG 2041
QY 1204 CCGCTGTGCTGCTTGGTTAATGATCGGTTGTCCGCTGCAATGGGTGCTCGGTTGAT 1263
Db 2042 CCGCTGTGCTGCTTGGTTAATGATCGGTTGTCCGCTGCAATGGGTGCTCGGTTGAT 2101
QY 1264 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY 1324 GGTGATTGGGCGGAGTGTGTTTCTTAG 1350

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Db 2162 GGTGATTGGCGGAGTGTTTTCCTTAG 2188
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RESULT 14
US-10-662-914-33
; Sequence 33, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-33
Query Match 99.7%; Score 1345.4; DB 17; Length 2665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CTGCGAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCGAGGCGATCAAA 63
Db 842 CTGCGAGTCCCGGCTCGAGAAATCAATCCAGTTGCGATACGGTTCGATCGAGGCGATCAAA 901
QY 64 TGCTTCTCCGAGACTTCGATCTTTGGGTCGATACGAGTTCGATCTCTCTGGCAAAAC 123
Db 902 TGCTTCTCCGAGACTTCGATCTTTGGGTCGATACGAGTTCGATCTCTCTGGCAAAAC 961
QY 124 GAATCGGTCAFTCCCTGAGGTCCCGCGGATGCGAGTCACTTTTCGTCAGGTCTCTC 183
Db 962 GAATCGGTCAFTCCCTGAGGTCCCGCGGATGCGAGTCACTTTTCGTCAGGTCTCTC 1021
QY 184 TCCCGTCAATGAGCGCGTATCCGACGACTCCGAGGCGAGAAATATGCTTCTCGAAGACATAC 243
Db 1022 TCCCGTCAATGAGCGCGTATCCGACGACTCCGAGGCGAGAAATATGCTTCTCGAAGACATAC 1081
QY 244 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAAATATGCTTCTCGAAGACATAC 303
Db 1082 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAAATATGCTTCTCGAAGACATAC 1141
QY 304 AACTACAGTTGGGTGAGATGACTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 363
Db 1142 AACTACAGTTGGGTGAGATGACTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 1201
QY 364 GGATCAAGTTCTACGAGCGGTAGCAATCGCTCAAGGAAACATCGTTCCATTCAATCCGA 423
Db 1202 GGATCAAGTTCTACGAGCGGTAGCAATCGCTCAAGGAAACATCGTTCCATTCAATCCGA 1261
QY 424 TCCTCTGGCTCCAGCGCGTATCGCTCCGCGAAGAAATTCATCGAGGCTTCAGAGC 483
Db 1262 TCCTCTGGCTCCAGCGCGTATCGCTCCGCGAAGAAATTCATCGAGGCTTCAGAGC 1321
QY 484 ACCAAGCTGAAGGATCCTCGTCCGACGCGGCAATCGTCGCGGAGATCGAGGTGTC 543
Db 1322 ACCAAGCTGAAGGATCCTCGTCCGACGCGGCAATCGTCGCGGAGATCGAGGTGTC 1381
QY 544 ATTTCCGAGGCGAGCTCATCCAAACACACTCTCGACCCAGGCACTGCACTGCTCTCGAA 603
Db 1382 ATTTCCGAGGCGAGCTCATCCAAACACACTCTCGACCCAGGCACTGCACTGCTCTCGAA 1441
QY 604 GACAGCAATGCGCGATACGTCGAGCAATTTACCCCGCAGTTCGTCCTCCCTCAAT 663
Db 1442 GACAGCAATGCGCGATACGTCGAGCAATTTACCCCGCAGTTCGTCCTCCCTCAAT 1501
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QY 664 CGTCAACGTTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAAGTGAACCTAC 723
Db 1502 CGTCAACGTTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAAGTGAACCTAC 1561
QY 724 CTCATGGACATGTCTCTTCGACACCATCTCCACGACACCGTTCGACACCGCTGCTCC 783
Db 1562 CTCATGGACATGTCTCTTCGACACCATCTCCACGACACCGTTCGACACCGCTGCTCC 1621
QY 784 CCCTTCTGACCTGTTTCAACCCATGACGAATGAATCAACTACGACTACTCTACGAGCTTTG 843
Db 1622 CCCTTCTGACCTGTTTCAACCCATGACGAATGAATCAACTACGACTACTCTACGAGCTTTG 1681
QY 844 AAAAGTATATAGCGCATGCTGTCAGTAACCGCTTCGCGCCGACCCAGCGGCTCGGCTAC 903
Db 1682 AAAAGTATATAGCGCATGCTGTCAGTAACCGCTTCGCGCCGACCCAGCGGCTCGGCTAC 1741
QY 904 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCTGTCCACGATGACACCAAGTTCACAC 963
Db 1742 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCTGTCCACGATGACACCAAGTTCACAC 1801
QY 964 CACACTTTGAGCTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1023
Db 1802 CACACTTTGAGCTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1861
QY 1024 TCGCATGACACGCGCATCATCTCCATTCCTTTGTTTAGTCTGTACAAACGCGACTAAG 1083
Db 1862 TCGCATGACACGCGCATCATCTCCATTCCTTTGTTTAGTCTGTACAAACGCGACTAAG 1921
QY 1084 CCGCTATCTACACGACCGTGGAGAAATATCAACCCAGACAGATGATGATTCCTGCTCTGG 1143
Db 1922 CCGCTATCTACACGACCGTGGAGAAATATCAACCCAGACAGATGATGATTCCTGCTCTGG 1981
QY 1144 AGGTTCCGTTTTCGCGTTTGTACGTCGAGATGATGACGTCAGTGTACGCGGAGGAG 1203
Db 1982 AGGTTCCGTTTTCGCGTTTGTACGTCGAGATGATGACGTCAGTGTACGCGGAGGAG 2041
QY 1204 CCGCTGGTCCGCTGTCTTGTTAATGATCGCGTTGTCGCGCTGCATGGGTGTCGCGTTGAT 1263
Db 2042 CCGCTGGTCCGCTGTCTTGTTAATGATCGCGTTGTCGCGCTGCATGGGTGTCGCGTTGAT 2101
QY 1264 GCTTTGGGAGATGTACCCGGGATGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1323
Db 2102 GCTTTGGGAGATGTACCCGGGATGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY 1324 GGTGATTGGCGGAGTGTTTTCCTTAG 1350
Db 2162 GGTGATTGGCGGAGTGTTTTCCTTAG 2188
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RESULT 15
US-10-662-914-15
; Sequence 15, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-15
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Query Match 99.5%; Score 1343.8; DB 17; Length 2665;

Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1345; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	4	CTGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTGGATATCAA	63
DB	842	CTGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTGGATATCAA	901
QY	64	TGCTTCTCCGAGACTTCGCACTTTGGGTCATTAACGACCGTTCTCTCTCTGGCAAC	123
DB	902	TGCTTCTCCGAGACTTCGCACTTTGGGTCATTAACGACCGTTCTCTCTCTGGCAAC	961
QY	124	GAATCGGTCACTCCCTCGAGTCCCGCGGATGCAAGTCACTTCGCTCAGGTCTTC	183
DB	962	GAATCGGTCACTCCCTCGAGTCCCGCGGATGCAAGTCACTTCGCTCAGGTCTTC	1021
QY	184	TCCGTCATGAGCGCGGTATCCGACCGACTCCAGGCGCAAGAAATCTCCGCTCTCAT	243
DB	1022	TCCGTCATGAGCGCGGTATCCGACCGACTCCCGGCGCAAGAAATCTCCGCTCTCAT	1081
QY	244	GAGGATCCAGCAGAACCGCACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC	303
DB	1082	GAGGATCCAGCAGAACCGCACCACTTTGACGGAATAATGCTTCTCTGAAGACATAC	1141
QY	304	AACATACGTTGGTGAGATGACTGACTCCCTTCGAGAACAGGAGTAGTCACTCC	363
DB	1142	AACATACGTTGGTGAGATGACTGACTCCCTTCGAGAACAGGAGTAGTCACTCC	1201
QY	364	GGCATCAAGTTCTACACCGGTGCAATCGCTCAAGGAACATCGTTCCATTCATCCGA	423
DB	1202	GGCATCAAGTTCTACACCGGTGCAATCGCTCAAGGAACATCGTTCCATTCATCCGA	1261
QY	424	TCCTTGCTCCAGCCGCTGATCGCTCCGCAAGAAATTCATCGAGGGCTCCAGAGC	483
DB	1262	TCCTTGCTCCAGCCGCTGATCGCTCCGCAAGAAATTCATCGAGGGCTCCAGAGC	1321
QY	484	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGCCCAATCGTCGCCCAAGATCGAGTGGTC	543
DB	1322	ACCAAGCTGAAGATCTCTGTCGCCAGCCCGCCCAATCGTCGCCCAAGATCGAGTGGTC	1381
QY	544	ATTTCCGAGGCGAGCTCATCAACAACTCTCAACCCAGGCACTGCACTGTCTTCGAA	603
DB	1382	ATTTCCGAGGCGAGCTCATCAACAACTCTCAACCCAGGCACTGCACTGTCTTCGAA	1441
QY	604	GACAGCAATTTGGCGGATACCGTGGAGCAATTTCAACCCAGGCTTCGCCCTCCATT	663
DB	1442	GACAGCAATTTGGCGGATACCGTGGAGCAATTTCAACCCAGGCTTCGCCCTCCATT	1501
QY	664	CGTCAACGCTGGAGAACGACCTGTCCGCTGTGACTCTCAAGACACAGAGTCACTAC	723
DB	1502	CGTCAACGCTGGAGAACGACCTGTCCGCTGTGACTCTCAAGACACAGAGTCACTAC	1561
QY	724	CTCATGGACATGTCTCTTGACACCACTCTCCAGCAGCCGTCGACACCAAGTGTCC	783
DB	1562	CTCATGGACATGTCTCTTGACACCACTCTCCAGCAGCCGTCGACACCAAGTGTCC	1621
QY	784	CCCTTCTGTGACTCTTCAACCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG	843
DB	1622	CCCTTCTGTGACTCTTCAACCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG	1681
QY	844	AAAAAGTATTACGGCCATGTGTGAGTAACCGCTTCGCCCGCAGCGGGGCTCGGTAC	903
DB	1682	AAAAAGTATTACGGCCATGTGTGAGTAACCGCTTCGCCCGCAGCGGGGCTCGGTAC	1741
QY	904	GCTACGAGCTCATCGCCGCTGACCCACTGCTGCTGCCAGATGACACCACTTCCAAC	963
DB	1742	GCTACGAGCTCATCGCCGCTGACCCACTGCTGCTGCCAGATGACACCACTTCCAAC	1801
QY	964	CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGACTTT	1023
DB	1802	CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACGCGACTTT	1861
QY	1024	TCGATGACACGAGCATCATCTCCATTCTCTTGGCTTTAGGTCTGTACAACGGCACTAAG	1083

DB	1862	TCGCATGACAAAGCGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAG	1921
QY	1084	CCGCTATCTACACGACCGTGGAGAAATATACCCAGACAGATGGATTCTCGTCTGCTTGG	1143
DB	1922	CCGCTATCTACACGACCGTGGAGAAATATACCCAGACAGATGGATTCTCGTCTGCTTGG	1981
QY	1144	ACGGTTCCGTTTCTTCGCTTTGATCGTCGAGATGATGATGATGATGATGATGATGATGAT	1203
DB	1982	ACGGTTCCGTTTCTTCGCTTTGATCGTCGAGATGATGATGATGATGATGATGATGATGAT	2041
QY	1204	CCGCTGCTCCGTTCTTCTGTTAAATGATCGCTTGTCCGCTGCAATGGGTGTCCGTTGAT	1263
DB	2042	CCGCTGCTCCGTTCTTCTGTTAAATGATCGCTTGTCCGCTGCAATGGGTGTCCGTTGAT	2101
QY	1264	GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG	1323
DB	2102	GCTTTGGGAGATGATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG	2161
QY	1324	GGTGGTTGGCGGAGTGTCTTCTTAG	1350
DB	2162	GGTGGTTGGCGGAGTGTCTTCTTAG	2188

Search completed: November 24, 2004, 13:02:13
Job time : 755 secs

Db 19 TGCACATAGTGTCAAGCTCGGATACCACTGCAACAGCCGTTTCTCAGCTCTGGGGCCAA 78
Qy 97 TAGCACCGCTTCTTCTCTGCGCAACGAATCGGTCACTCCCTCAGGTGCGCCGCGGA 156
Db 79 TATTCCCCCTATTCTTCTCTGAAGTCAAGTCTCCCATCTCTCCGATGTACCGTCTGGA 138
Qy 157 TGCAGAGTCACTTCGCTCAGTCTCCTCTCCGTCATGGAGCGGCTATCCGACCGACTCC 216
Db 139 TGCACATATTACTTTTGCCCAAGTCTCTCCGATGGAGCAAGGTATCCCAAGAAAG 198
Qy 217 AAGGCAAGAAATACCTCGCTCTCATTGAGGAGATCCAGCAGAACCGACCACTTTGAC 276
Db 199 AAAACCGAGCTACGCAAACTCTTTGATCGGATCAAGGAACCAAGCAAGTCTTATGAG 258
Qy 277 GGAATAATGCTTCTGTAAGACATCAACTCAGCTTGGGTGCAATGACCTGACTCCC 336
Db 259 GACGACTTCAAGTTCTCTGAAAAAATTTGAGTATACGCTGAAGAGCGATGATATGACAGAA 318
Qy 337 TTCCGGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTTACCAGCGGTACGAATCGCTC 396
Db 319 TTCCGGGAACACCACTCTTCAATTTCTGGGGCAAAATTTCTACGATCGCTATAGGGGTTG 378
Qy 397 ACAAGGAACATCGTTCATTCATCCGATCCTCTGGCTCCAGCCGCGTGATCGCTCCGGC 456
Db 379 GCGAAGGAGATACGACCGCTTCTGTCGAGCTGCGGGCTCTCCGAGGGTGATCAAGTCAGCA 438
Qy 457 AAGAAATTCAGAGGCTTCCAGAGCACCAAGCTGAAGATCCTCGTGCCCAAGCCGCGC 516
Db 439 GAGAGATTATTCAAGGATCCAGAGTCTTGGGCTTGATCTGATGGTGTGGAAG 498
Qy 517 CAATCGTCGCGCAAGATCGAGTGGTCAATTTCCGAGGCCAGCTCATCCAAACAATCTTC 576
Db 499 GATAGACCCCTATTCGTCAACTTGATTTATCCCTGAAGGAGTCCGAGTAACAATACACTT 558
Qy 577 GACCCAGCACCTGCTCTTCCGAGACAGCAATTTGCCCGATACCGTTCGAAGCCAAT 636
Db 559 GACCACTCTTTATCGGAAAACTTCGACACGGAATTTTCAGGAAAGAGAGACGAAAAAA 618
Qy 637 TTACCCGCGAGTTGCTGCTCCCTCCATTCGTCACAGCTGTGAGAACGACCTGTCCGGTGTG 696
Db 619 TTCTGGACCTATTGTCCTCCCTCCAAATTTTGAGCGTGTGAAATCATCTCTCCCTGGCGC 678
Qy 697 ACTCTCAGACAGCAAGTGAACCTACTCATGACATGTGCTCTTCGACACCATCTCC 756
Db 679 AATATTACGCTCAGAGATGTATCTACTCATGGATATGTGCTCTTCACACCGTGATG 738
Qy 757 ACCAGCACCGTCGACACCAAGCTGTCCCTCTCTGTGACCTGTTTCAACCCATGACGAATGG 816
Db 739 TTGAGCGCCGAGCGGACCAACTATCTCCATTTCTGCCAATCTTTCACCCCGAGCGATGG 798
Qy 817 ATCAACTACGACTACCTCCAGTCTCTTGAAGAAATTTACGGCCATGGTGAGTAACCCG 876
Db 799 GTTGACTATGACTACTACCACTCTCTTGGGAAATATTACAGATATGGGGCCAGGACCCG 858
Qy 877 CTCGGCCGACCCAGGGCGTGGCTACGTAACGAGCTCATCGCCGCTCTGACCCACTCG 936
Db 859 CTCGGTGTGAGCAAGGATGGGATTCACCAACGAATCTATAGCCCTCTCAACAACACC 918
Qy 937 CCTGTCCACGA 947
Db 919 CCCGTCAATGA 929

RESULT 2
CO011644
LOCUS
DEFINITION
EST799979 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEB041 5' end, mRNA sequence.
ACCESSION
CO011644
VERSION
CO011644.1 GI:48518533
KEYWORDS
EST.
Coccidioides posadasii
SOURCE
Coccidioides posadasii
ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 810)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
Unpublished (2003)
Other ESTs: EST799978
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1..810
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIEB041"
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/clone_lib="Coccidioides posadasii spherule cDNA library,
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/note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

ORIGIN

Query Match 19.9%; Score 268.6; DB 7; Length 810;
Best Local Similarity 59.6%; Pred. No. 1.8e-62;
Matches 476; Conservative 0; Mismatches 314; Indels 9; Gaps 1;
Qy 524 CGCCAAAGATCGAGTGTGTCATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAG 583
Db 1 CCCCTATCGTCAACTTGATTTATCCCTGAGAGAGTGGAGTAACAATACACTTGACCACT 60
Qy 584 GCACCTGCATCTGTTTGAAGACAGCGAATTTGGCCGATACCGTCGAAGCCCAATTTACCG 643
Db 61 CTTTATGCGAAAACTTTCGAACAGGATATTCAGGAAAGAGAGACAGAAAAAATTCGTGG 120
Qy 644 CCAGCTCGTCCCTCCATTCGTCACAGCTCGGAGAACGACCTGTCCGGTGTGACTCTCA 703
Db 121 ACCTATTTGCCCTCCAAATTTTGAGGTGTGAAAATCATCTCCCTGGGCCATATTA 180
Qy 704 CAGACACAGAAAGTACCTACCTCATGGACATGTCTCCTTCGACACCATCTCCACCAAGCA 763
Db 181 CGGTACACAGATGTGATCTACCTCATGGATATGTCTCTCCACACCGTGATGTTGACGC 240
Qy 764 CGGTGACACCAAGTGTCCCTCTCTGTGACCTGTTCCACCCATGACGAAATGGATCAACT 823
Db 241 CGAGCGCAGCAAACTATCTCCATTTCTGCCAACTCTTCACCCAGGCGAATGGGTTGACT 300
Qy 824 ACGACTACTCTCCAGTCTTGAAGAAATTTACGGCCATGTGTGAGTAACCCGCTCGGCC 883
Db 301 ATGACTACTACCACTCTCTTGGGAAATATTACAGATATGGCCAGGACGCCGCTCGGTG 360
Qy 884 CGACCCAGGGCGTGGCTACGCTAACGAGCTATCGCCCTCTGACCCACTCGCGCTGCTCC 943
Db 361 CTGAGCAAGGATGGGATTCACCAACGAATCATAGCCCGTCTCACAAACACCCCGCTCA 420
Qy 944 ACGATGACACAGTTCACCAACCACTTTGGGACTCGAGCCCGGCTACCTTTCCGCTCAACT 1003
Db 421 ATGACTCGACTTCCACCAACCGGACTCTTACTCTCACCCTGACCCACTTCCCGCTAAAG 480
Qy 1004 CTACTCTCTACCGGACTTTTCGATGACCAAGGCAATCATCTCCATTTCTTTGCTTAG 1063
Db 481 CCATCTCTACGCACTTCAGCCATGATAACACTATGATAACGATCTTTCACGCCCTTGG 540
Qy 1064 GTCTGTAACGGGCACTAAGCGGTATCTACCAGCGGTGAGAAATATACCCAGACAG 1123


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CO011643/c
LOCUS      737 bp      mRNA      linear      EST 09-JUN-2004
DEFINITION Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
            kb Coccidioides posadasii cDNA clone CIEB041 3' end, mRNA sequence.
ACCESSION  CO011643
VERSION     CO011643.1
KEYWORDS    GI:48518532
SOURCE      Coccidioides posadasii
            Cocciidioides posadasii
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE   1 (bases 1 to 737)
AUTHORS     Gardner,M.J. and Cole,G.T.
TITLE       Analysis of gene expression in Coccidioides posadasii mycelia and
            spherules via expressed sequence tags
JOURNAL     Unpublished (2003)
COMMENT     Other ESTs: EST799979
            Contact: Gardner MJ
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.

FEATURES             source
     1..737
     /organism="Coccidioides posadasii"
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     /strain="C735"
     /db_xref="taxon:199306"
     /clone="CIEB041"
     /dev_stage="spherules"
     /lab_host="E. coli DH10B, Tl phage resistant"
     /clone_lib="Coccidioides posadasii spherule cDNA library,
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     /note="vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
     Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
     kb"

ORIGIN
Query Match      15.1%; Score 203.8; DB 7; Length 737;
Best Local Similarity 61.0%; Pred. No. 1.2e-44;
Matches 353; Conservative 0; Mismatches 217; Indels 9; Gaps 1;

QY      781  TCCCCCTCTTGTGACCTCTTCAACCATCACGAATGGATCAACTACGACTACTCTCCAGTCC 840
DB      737  TCTCCATTCTGCCAACTCTTCAACCCAGCGAATGGGTGACTATGACTACTACAGTCT 678

QY      841  TTGAAAAAGTATTACGGCCATGGTGCAGTTAAACCGCTCGGCCGACCCAGGGGTGCGC 900
DB      677  CTTGGGAATAATTACAGATATGGGCCAGGCGCGCTCGGTGTGACCAAGGCATGGGA 618

QY      901  TACGGTAACGAGCTCATCGCCGCTGTGACCCACTCGCCTGTCCACGATGACACAGTTCC 960
DB      617  TTCACACAGAACTCATAGCCGCTCTCAACACACCCCGTCATGATGATCGACTCCACCC 558

QY      961  AACCAACATTGGAGTCGAGCCCGGCTACCTTTCCGCTCAACTCTCTCTCTTACGCGGAC 1020
DB      557  AACCAGCACTTTACCTCTCACGCCGACCACTTCCCGCTTAAACGCCACTCTCTACGCGAC 498

QY      1021  TTTTCGGATGACACGGGATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAAAGGCACT 1080
DB      497  TTCAGCCATGATAAACAATGATTAACGATCTTACGGCTTTGGGGCTGTTCAATAGACG 438

QY      1081  AAGCCGCTACTTACACGACCGGTGAGAAATATCACCCAGACAGATGGATTCTCTGTGCT 1140
DB      437  GAACCACTCCCCCTTACCGCATCCGACCCCGGTAGAGTCGGACCGATTCTTCCGCTCG 378

QY      1141  TGGACGGTTCCGTTTGGCTTTCGGTTTGTACGTTCGAGATGATGCACTGTCCAGCGGAGC-- 1198
DB      377  TGGACGGTCCCGTTTGGCGGTAGGGCTTACGTTCGAGAAATGAAGTGTGATGTTGTCGCA 318

QY      1199  -----AGGAGCCGCTGCTCGTCTCTTGGTTTAAATGATCGCGTTGTCCCGCTCATGGG 1251
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Query Match 12.3%; Score 165.6; DB 1; Length 603;
Best Local Similarity 59.8%; Pred. No. 3.6e-34;
Matches 298; Conservative 0; Mismatches 194; Indels 6; Gaps 1;
QY 779 TGTCCTCCCTCTGTGACCTGTCACCATGACGAATGGATCAACTAGACTACTCCAGT 838
Db 106 TCTCTCCATTTGGCAATATTAAGTCTGCTGAAATGGCGGCTAGATTACTACAAA 165
QY 839 CTTTGAATAAGTATTACGGCCATGTTGCAAGTAAACCGCTGCGCCGACCCAGGGCGT 898
Db 166 CAGTTGGAAGTACTACGGCTATTTCATGGGGTAAATCCACTCGACCACTCAGGGCGT 225
QY 899 GCTACGCTACAGCTCATCGCGCTGACCACTGCGCTGTCACGATGACACAGTT 958
Db 226 GTTTTACTAATGAGCTAATTGCAAGTCACTCGCTCTCCGCTCATCGATCAGACGA 285
QY 959 CCAACCACTTTGCACTCGAGCCGCTACTCTTTCGGCT-----CAACTCTACTCTCT 1012
Db 286 CTAATAACACACTGACACAAATCCAGGAGTTTCTCTCGATAGCAAACTGCTCTT 345
QY 1013 ACGCGGACTTTTCGATGACAAAGGATATCTCCATCTCTTTGCTTAGTCTGTACA 1072
Db 346 ACGCGGACTTTAGCCAGCAACAGCTCACTAGCATATTGGCTGCGAGTTGGTCTCTACA 405
QY 1073 ACGGCACTAGCGCTACTACCAAGCGTGGAGATATACCCAGACAGATGGATTCT 1132
Db 406 AATTTCTCCGCACTCTCAAGACGAGCTCAATTTTACGGGACGATGACTATT 465
QY 1133 CGTCTGCTTGACGCTTCGCTTTCCTTTGCTTTGATGCTGAGATGATGATGCTGAGG 1192
Db 466 CGACTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
QY 1193 CGGAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252
Db 526 ATGTACGCGAAGATATGATGCGGATCTTGTGAATGATGCGGCTTCTCCACTTCAATCT 585
QY 1253 GTCCGGTTGATGCTTTGG 1270
Db 586 GTGCGGAGATGCAATGG 603

RESULT 8
AQ324539/c 802 bp DNA linear GSS 08-JAN-1999
LOCUS mgxb0019C01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
DEFINITION clone mgxb0019C01r, genomic survey sequence.
ACCESSION AQ324539
VERSION AQ324539.1 GI:4116391
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 408.
Location/Qualifiers
1..802
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"

/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0019C01r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 11.5%; Score 155; DB 8; Length 802;
Best Local Similarity 57.3%; Pred. No. 3.1e-31;
Matches 303; Conservative 0; Mismatches 220; Indels 6; Gaps 1;
QY 773 CCAAGCTGTCCTCCCTCTGTGACCTGTCACCATGACGAATGGATCAACTAGACTACTC 832
Db 537 CCACCTGTCGAGTTCGACGCTTTACGCAACGAGACTGGGAGGATATGACTATC 478
QY 833 TCCAGTCTCTGAAAAGTATTACGCGCATGTGTGAGGTAAACCGCTGCGCCGACCCAGG 892
Db 477 TCCAGACTGGGNAAGTGGTATGGTACGGCAATGGCAACCCCTGGCTCCACGCAAG 418
QY 893 GCGTCGGTACGTAAACGAGCTCATGCGCCCTGTGACCCACTGCGCTGTCACGATGACA 952
Db 417 GGGTGGCTTCTGTCACGAGCTCATGCGAGGCTGCTCCAAAAGCCCGTTGAAGACACA 358
QY 953 CCAGTTCCAAACACACTTTGGACTCGAGCCGCTGACTCTTCGGCTCAACTCTACTCTCT 1012
Db 357 CAAATACCACTCGACGCTCGACGACCCATCGAGCTTCCACTAGACAAAAGCTGT 298
QY 1013 ACGCGGACTTTTCGATGACAAAGGATCATCTCCATTTCTTTGCTTTAGTCTGTACA 1072
Db 297 ACGCGGACTTTAGCCATGATAAGATATGCTGGGCATCTAGCGCGCTGGGGATTTACA 238
QY 1073 ACGGCACTAAGCGCTATCTACCAAGCGTGGAGATATACCCAGACAGA-----TG 1126
Db 237 ACGGCAAGCGCCCGGATTCGGTCCCAAAAAGGAGAGAGAGCGGCGGAGGCTCAGCG 178
QY 1127 GATTCTCGTCTGTTGGACGCTTCGGTTCGCTTTCGCTTTCGCTTTCGCTGAGATGATG 1186
Db 177 GGTTCGTCGAGTGGCGGTTACCGTTCGAGCGAGGATGTTTGTGAAAAATGACTT 118
QY 1187 GTCAGCGGAGCAGAGCGCGCTGGTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1246
Db 117 GCGCAGGCGGAGAACGAGGAGCTTTGTGAGATCTCTGTCACGACGAGGTTGAGCGCGCTGC 58
QY 1247 ATGGGTGTCGCTGTCATGTTTGGGAGATGATGACCCGGGATAGCTTTGT 1295
Db 57 AGAACTGCGATCCGACACATGAGTGGTTCGTCACGCTGAGCAAGTCTGT 9

RESULT 9

CD031252 620 bp mRNA linear EST 07-MAY-2003
LOCUS mgmt005xE03f.b Mated culture Magnaporthe grisea cDNA clone
DEFINITION mgmt005xE03 5', mRNA sequence.
ACCESSION CD031252
VERSION CD031252.1 GI:30413088
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaportha.
1 (bases 1 to 620)

AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
 Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe
 grisea
JOURNAL Unpublished (2002)
COMMENT Contact: Ebbole DJ
 Department of Plant Pathology & Microbiology
 Texas A&M University
 Peterson Bldg, WS2132, College Station, TX 77843-2132, USA
 Tel: 979 845 4831
 Fax: 979 845 6483
 Email: d-ebbole@tamu.edu
 Chromatogram file of this sequence is available, see contact
 person; Best nr hit (April, 22, 2003) gb|AB52508.1| phytase
 [Chielavia heterothallica] 239 3e-62
PCR Primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgmt005 row: E column: 03
 Seq primer: T3.

FEATURES

source	Location/Qualifiers
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	/sex="Mat1-2 and Mat1-1 mixed culture"
	/cell_type="mixed sexual development"
	/dev_stage="asci, ascospores, Perithecia, mycelium"
	/clone_lib="Mated culture"
	/note="vector: pBluescriptSK; Site1: EcoRI; Site2: XhoI;"
	Two mating types were co-cultivated over a filter paper on oatmeal agar medium. After three days at 25 C plates were transferred to 21 C. Perithecia with asci and ascospores formed at the beginning of the third week. Material was collected by scraping tissue from the filter paper..
	Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match	11.2%;	Score 150.8;	DB 6;	Length 620;
Best Local Similarity	55.1%;	Pred. No. 4.3e-30;		
Matches 343;	Conservative 0;	Mismatches 267;	Indels 12;	Gaps 2;

QY 567 CAACACCTCTCGACCAGGCACCTGCATCTGTTCTTCCAGACAGCGCAATTGCCGATACCGT 626
 Db 1 CAACACGCTAAACCAATACCACTATGTACTGCTTTGAGAACACCAAACTCGCAGAGAGC 60
 QY 627 CGAAGCCAAATTACCCGCCAGTTGCTGCCCTCCATTCGTCACGCTGTGAGAACGACCT 686
 Db 61 CCAAAAGGAGTTTATGAGAGAGTGCAATGGCGGCATACAGAGCGCTTGAAACACGCGCT 120
 QY 687 GTCGGGTGTCACTCTCACAGACACAGAAAGTGACCTACTCATGACATGTGCTCTTCGA 746
 Db 121 GGAGGTGCAAACTCAGACCACAGACGGGTGCAGATCATGGAGCTTGCCTGTTGA 180
 QY 747 CACCATCTCCACAGACACCGTCGACACCAAGCTGTGCCCTTCTGTGACCTGTTACCCA 806
 Db 181 GACCGTGGCAGATCCCCAAG-----CCACCCCTGTCGAGTTCTTCGACGCTGTTACGCA 234
 QY 807 TGACGAATGATCAACTACGACTACCTCCAGTCCCTTCAAAAAGATTATACGGCCATGTGC 866
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 QY 867 AGGTAACCCCGTCGGCCCGACCCAGGGCGTTCGGTACGCTAACGAGCTATCGCCCGTCT 926
 Db 295 TGGCAACCCCGTGGGCTCCACGGAAGGGGTGGGTTCCGTCAACGAGCTCATCGAGGCT 354

QY	927	GACCCACTCGCCTGTCCACGATGACACCAAGTTCCTCAACACACACTTTGGAATCTGAGCCCGGC	986
Db	355	GCTCCAAAAGCCGGTTGAAGACACACAAATACCACTCGACGCTCGACAGCGACCCATC	414
QY	987	TACCTTTCGCTCAACTCTACTCTCTACGCGGACTTTTCGATGAGAACGGCATCATCTC	1046
Db	415	GAGTTCCTCCACTAGACAAAAGCTGTACGCGGACTTTAGCCATGATACCATATGCTGGG	474
QY	1047	CATTCTCTTTTGGCTTTAGGTCTGTACAAACGGCCTAAAGCCGCTATCTACCAACGACCGTGA	1106
Db	475	CATCTACGCGCGCTGGGGATTTTACAAGCCACCGGCCCGGATTCGGTCCCAAAAAGGA	534
QY	1107	GAATATCACCCACACAGA-----TGGATTCTTCGTCTGTCTGACGCTTCGGTTCCGTTTC	1160
Db	535	GAGAGAGCGCGCAGGAGCTACAGCGGTTCTCGGCCAGCTGGCGGATACCGGTCGACG	594
QY	1161	CGCTTTTGATCTCGAGATGATG	1182
Db	595	GAGGATGTTTGGTGAAAAAGG	616
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CF882569/c			
LOCUS			
DEFINITION	CF882569	544 bp mRNA linear EST 31-OCT-2003	
	trio030xn08.g1 T.reesei mycelial culture, Version 6 October 2003		
ACCESSION	CF882569	Hypocrea jecorina cDNA clone trio030xn08, mRNA sequence.	
VERSION	CF882569.1	GI:38137251	
KEYWORDS		EST.	
SOURCE		Hypocrea jecorina (anamorph: Trichoderma reesei)	
ORGANISM		Hypocrea jecorina	
REFERENCE		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
AUTHORS		Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.	
		1 (bases 1 to 544)	
		Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,	
		Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,	
		Ward, M. and Dean, R.A.	
TITLE		Characterization of the protein processing and secretion pathways	
		in a comprehensive set of expressed sequence tags from Trichoderma	
		reesei	
JOURNAL		FEMS Microbiol. Lett. 230 (2), 275-282 (2004)	
COMMENT		Contact: Ralph A. Dean	
		Fungal Genomics Laboratory	
		North Carolina State University	
		Campus Box 7251, Raleigh, NC 27695, USA	
		Tel: 919-513-0020	
		Fax: 919-513-0024	
		Email: ralph.dean@ncsu.edu	
FEATURES		Seq primer: Lr-R1 primer.	
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		/clone_lib="T.reesei mycelial culture, Version 6 October	
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		and Nitrogen sources and concentrations."	
ORIGIN			
Query Match		10.3%; Score 138.4; DB 7; Length 544;	
Best Local Similarity		57.7%; Pred. No. 1.1e-26;	
Matches 247; Conservative		0; Mismatches 181; Indels 0; Gaps 0;	
QY	914	TGATCGCCCGTGCACCCACTCGCCTGTCCAGATGACACCAAGTTCACACACACTTTGG	973
Db	544	TGATTCCCAAGCTGACGGCGAGCCTGTGCAGATCGCAGCAGCAGACAGACACTCG	485
QY	974	ACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTTTCGATGACA	1033

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484 ACTCTTCCACCGCAGACGCTTCCCTCGACGCCAAGCTGTACGCCGAGCTTTTCGCACGACA 425
QY 1034 ACGCATCATCTCCATCTCTTTGCTTTAGGTCTGTACACGCGCACTTAAGCCCTATCTA 1093
Db 424 ACACATGTCTTCCATTTTTCGGCCCTTGGGCATGTTCAACTGCACAGGATCTGCCGC 365
QY 1094 CCACGACCGTGGAGAATATACCCACAGACAGATGATTTCTGTGTGTGACCGGTTCCGT 1153
Db 364 TCAAGTACAAGCTGTCTCCCAAGAAGCTTCACGGCTTCTCCGGTCTGTGGTCTGTCCGT 305
QY 1154 TTGCTTCGGCTTTGCTAGTGCAGATGATGAGTCTCAGCGGAGCGAGGACCGCTGTCTC 1213
Db 304 TTGTGCGCCGATGATGCTGGAGAGATGAGTGCAGCGGCTGCAGAGCCCTGTGTC 245
QY 1214 GTGCTTTGGTTAATGATCGGCTTGTCCGCTGCATGCGGTGTCCGGTTGATGCTTTGGGA 1273
Db 244 GGATCATCTCAACGACCGGCTGTGCGATGCGGAGCTGCAACTCGGACTCGGCTGGGC 185
QY 1274 GATGTACCGGGATAGCTTTGTAGGGGGTTGACCTTTGCTAGATCTGGGGGTGATGGG 1333
Db 184 GGTGCAAGCTGGGTGCTTTTATTGATAGCTGACGTTGTGCGCGGAGGGGCTGTGGA 125
QY 1334 CGGAGTGT 1341
Db 124 ATCAGTGT 117

RESULT 11
AJ274007 581 bp mRNA linear EST 29-DEC-1999
LOCUS AJ274007 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae
DEFINITION cDNA clone Ma#1628, mRNA sequence.
ACCESSION AJ274007
VERSION AJ274007.1 GI:6433380
KEYWORDS EST.
SOURCE Metarhizium anisopliae
ORGANISM Metarhizium anisopliae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
REFERENCE 1 (bases 1 to 581)
AUTHORS Screen,S.E., Mathur,P. and St. Leger,R.J.
TITLE EST analysis of the insect pathogenic fungus Metarhizium anisopliae
JOURNAL Unpublished (1999)
COMMENT Contact: Screen SE
Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA.
FEATURES
source
1. 581
/organism="Metarhizium anisopliae"
/mol_type="mRNA"
/strain="ARSEF 2575"
/db_xref="taxon:5530"
/clone="Ma#1628"
/clone_lib="Metarhizium anisopliae ARSEF 2575"
/note="Vector: Unizap; Metarhizium anisopliae was grown on insect cuticle for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector, Unizap"

ORIGIN
Query Match 8.7%; Score 117.6; DB 1; Length 581;
Best Local Similarity 55.0%; Pred. No. 5.7e-21;
Matches 275; Conservative 0; Mismatches 219; Indels 6; Gaps 2;

QY 2 TGCTGGCAGTCCCGCTCGAGAAATCAATCACTTCGATAGCTCGATCGATCGAGGGTATC 61
Db 77 TTCTGGGCTTGGCTTTCGGCGAGATGATCACTCAAGTCAATGCTTAAACACGGCT 136
QY 62 AATGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGCTTTCTCTCTGCGAA 121
Db 137 CCTGCACCCAGATTTTCGCAACACTGGGGCCAGTACTCGCGGTACTTCTCTC---AGCAC 193

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122 ACGAATCGGTCACTCTCCCTGAGTGGCCGCGGATGAGAGTCACTTTGCTCAGGTCC 181
Db 194 ACAAGGGATCTATTAAAGCTGACATCCCGTCGGGATCGAGGTACCTTTGCTTCAATCT 253
QY 182 TCTCCGTCATGAGCGCGGTATCCGACGACTCCAGGGCAAGAAATATCTCCGCTCTCA 241
Db 254 TGTCTGACATGGTCCCGCAACCGACGGCCGCAAGTCCCAAGCCCTACAAGACCTGG 313
QY 242 TTGAGGAGATCCAGCAGAACCGCACCTTTTGACGGAAATATGCGTTCTCTGAAGACAT 301
Db 314 TTGAGCGGATCCAAAAAGACGCTCAAGGACTATGGAAGGGCTTCGAGTTTCTCAAGATT 373
QY 302 ACACTACAGCTTGGGTGCAGATGACCTGCTCCCTTCGGAGAACAGAGTACTCAACT 361
Db 374 ACAAGTATCTCTAGGTCTGACGACCTCACCCCTTGGGCGAGCAGAAATGTCAGT 433
QY 362 CGGCGATCAAGTTTCTACCGCGGTACGAATCGCTCACAAAGGAA---CATCGTTCCATTCA 418
Db 434 CTGGAABAAAGTTCTTCAAGCGCTATCAGAAGTTAGCGGAGATTTCGACCATCCCTTG 493
QY 419 TCGATCTCTGCTCCAGCGCGGTGATCGCTTCGGCAGAGAAATTCATCGAGGCTTCC 478
Db 494 TTCGAGCCTCGGGCTCTGAAAGAGTCGTCATGTCAGCGCAAGATTTCATGCGCTTCT 553
QY 479 AGAGCACCAAGCTGAAGGAT 498
Db 554 ACAAGCCCAAGGCCAAGAAAT 573

RESULT 12
CN808226 1059 bp mRNA linear EST 27-MAY-2004
LOCUS CN808226 Blood EST0309 Metarhizium anisopliae ARSEF 2575 from insect blood
DEFINITION Metarhizium anisopliae cDNA clone B688 5', mRNA sequence.
ACCESSION CN808226
VERSION CN808226.1 GI:47729699
KEYWORDS EST.
SOURCE Metarhizium anisopliae
ORGANISM Metarhizium anisopliae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
REFERENCE 1 (bases 1 to 1059)
AUTHORS Wang,C.S., Hu,G. and St. Leger,R.J.
TITLE Gene expression profiling of Metarhizium anisopliae grown under different conditions: mechanisms of fungal opportunism
JOURNAL Unpublished (2004)
COMMENT Contact: Wang CS
Department of Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA
Email: cwang4umd.edu
Seq primer: M13 Reverse.
FEATURES
source
1. 1059
/organism="Metarhizium anisopliae"
/mol_type="mRNA"
/db_xref="taxon:5530"
/clone="B688"
/clone_lib="Metarhizium anisopliae ARSEF 2575 from insect blood"
/note="Vector: pCMV.SPORT6.1; Metarhizium anisopliae was grown in insect haemolymph for 24 hours. A cDNA library was constructed in the vector pCMV.SPORT6.1"

ORIGIN
Query Match 8.7%; Score 117.6; DB 7; Length 1059;
Best Local Similarity 55.0%; Pred. No. 6.5e-21;
Matches 275; Conservative 0; Mismatches 219; Indels 6; Gaps 2;

QY 2 TGCTGGCAGTCCCGCTCGAGAAATCAATCACTTCGATAGCTCGATCGATCGAGGGTATC 61

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napus Cultivar: Expressed Sequence Tag Analysis Identifies Genes
Associated with Fungal Pathogenesis
Fungal Genet. Biol. 41 (8), 735-753 (2004)
Contact: Hegedus D.
Agriculture & Agri-Food Canada
107 Science Place, Saskatoon, Canada, S7N 0X2
Email: hegedusd@agr.gc.ca
Insert Length: 520 Std Error: 0.00.
Location/Qualifiers
1. 520

FEATURES

Source
/organism="Sclerotinia sclerotiorum"
/mol_type="mRNA"
/strain="100"
/db_xref="taxon:5180"
/tissue_type="mycelia"
/lab_host="E. coli"
/clone_lib="SS pectin"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Sclerotinia sclerotiorum (strain 100) was
inoculated into minimal salts citrus pectin medium and
allowed to grow for 10 days at room temperature prior to
harvest. Single pass sequencing was done using the T3
(ATTACCTCACTAAAGGA) and T7 primers
(TAATACGACTCACTATAGG)."

ORIGIN

Query Match 8.5%; Score 114.2; DB 6; Length 520;
-Best Local Similarity 59.9%; Pred. No. 4.8e-20;
Matches 191; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY 1030 GACAAACGACATCTCCATCTCTTTCTTAGTCTGTACAAACGCGACTTAACCGCTA 1089
DB 2 GACAATGACATGACTGCTATATCTCCGCTCTTGGTCTGTATACTCCACAAGCGCATTA 61
QY 1090 TCTACACGACCGTGGAGATATACCCAGACAGATGATTTCTGCTGTGACCGTT 1149
DB 62 TCAAAACGAGAGAGATGCGTGTGCAACGAGTGGCTATTACGCGAGTTGTCGGTA 121
QY 1150 CGTTTGGCTTCGCGTTTGTAGTGTGAGATGATGACGATGTCAGGCGGAGCAGGCGCGCTG 1209
DB 122 CCAATTGACGAGGATGTATGTGAGAGATGACCTGTGCGGTGAGATGAGAGTTG 181
QY 1210 GTCCGTGCTTGGTTAATGATCGGTTGTCCGCTGCAATGGGTGTCGCGTTGATGCTTTG 1269
DB 182 GTTAGAGTTATGTTAATGACCGCGTGTCTACAANTAAAGACATGTGTTGGTGAATG 241
QY 1270 GGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGGGGTGAT 1329
DB 242 GCGAGATGTGATGTCAAGTTTGTAGAGATTTGAGCTTTGCTAGTGAAGGGGTGAC 301
QY 1330 TGGGGGAGTGTGTTGCTT 1348
DB 302 TGGGGAGCTGCTTTACTT 320

RESULT 15
LOCUS AQ255459 837 bp DNA linear GSS 23-OCT-1998
DEFINITION mgxb0014M15r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0014M15r, genomic survey sequence.
ACCESSION AQ255459
VERSION AQ255459.1 GI:3779774
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 837)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)

COMMENT

Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: PAC ends
High quality sequence start: 60
High quality sequence stop: 277.

FEATURES

Source
1. 837
/organism="Magnaporthe grisea"
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/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0014M15r"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBRACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 8.0%; Score 107.6; DB 8; Length 837;
Best Local Similarity 53.6%; Pred. No. 3.5e-18;
Matches 224; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
QY 662 TTCTGCAACGCTGCGAGAACGACCTGTCGGGTGCTGACTCTCACACACACAGAGTACCT 721
DB 119 TTATACACGCTAGCTGGGATTTTCAAGTGTGGGTAAACCGTCAAGACGTTGTAA 178
QY 722 ACCTCATGACATGTGCTCTTTCGACACCATCTCCACCAGCACCGTCCGACACCAAGCTGT 781
DB 179 ATCTTATGGGACTGTGCACCATGGAACCAACGCGCAACTTTGAAAAAACTGCGCAACTT 238
QY 782 CCCCCTTCTGTGACCTGTTCCACCATGACATGATGATCACTACCTACCTCCAGTCTCT 841
DB 239 CACCCCTTTGCACTGTTTACGGAAGCAGATTTGGTAAATATATGTTTACTTGTCCACGG 298
QY 842 TGAAAAAGTATTACGCCCATGGTGCAGGTAAACCCGCTCGGCCCGACCCAGGGCGTCCGCT 901
DB 299 TGCAAAAATGGTACAGATACGGAACCGGTATCTTTTGGGCCCACTATGCGCGTGGGAT 358
QY 902 ACGCTAACGAGCTCATCCCGCTGTGACCCACTGCGCTGTCCAGATGACACCAAGTCCA 961
DB 359 GGGTAAACGACTTATTTCAGCATTTAACCCGAAAGCCAGTCCAAAGATCAAAACCATGTCCA 418
QY 962 ACCACACTTTGGACTTCGAGCCCGGCTACTTTCCGCTCAACTTACTCTCTACCGGACT 1021
DB 419 ATACGACACTTGCATGAAACCCGGAACTTACTCTTACAGGCAATTTGATGCTGATT 478
QY 1022 TTTCGATGACAAACGCGATCATCTCCATCTCTTTGCTTTAGGCTGTGTACACGCGAC 1079
DB 479 TTATCCATACGAGCAGATATTATAGGATTTACGCGCGGTTTGGGCTATTTAACGCCCC 536

Search completed: November 24, 2004, 11:09:45
Job time : 4738 secs